wwPDB EM Validation Summary Report

Mar 8, 2026 – 04:19 PM UTC

PDB ID	:	9BUS / pdb_00009bus
EMDB ID	:	EMD-44918
Title	:	Single particle CryoEM structure of the Pf80S ribosome in the unloaded state (nrt with E-site tRNA)
Authors	:	Anton, L.; Haile, M.; Ho, C.M.
Deposited on	:	2024-05-17
Resolution	:	2.40 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references ⓘ) were used in the production of this report:

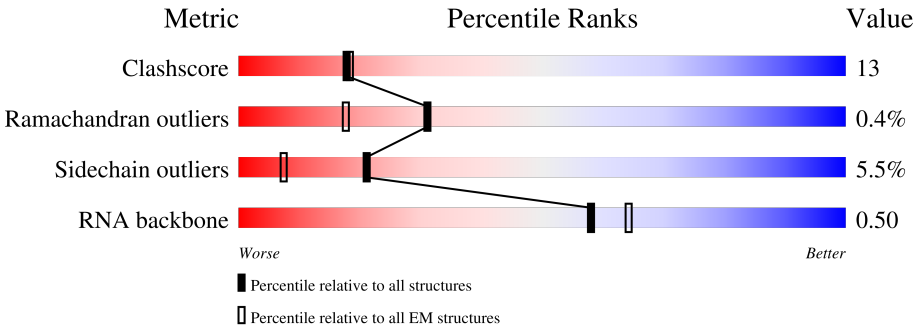
EMDB validation analysis	:	0.0.1.dev132
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

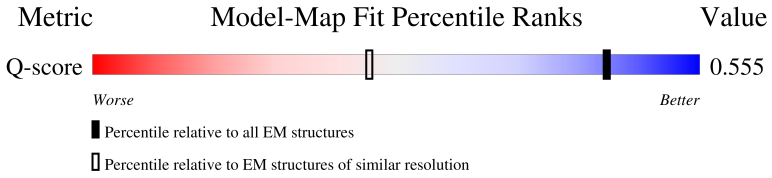
1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.





Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	5628 (1.90 - 2.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	S1	133	50% 38% • 10%
2	S2	105	29% 29% 10% 61%
3	S3	107	57% 32% 11%

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Mol	Chain	Length	Quality of chain
4	S4	82	7% 50% 41% 7%
5	S5	67	6% 43% 42% 12%
6	S6	58	45% 28% 26%
7	S7	74	24% 62% 14%
8	SA	2092	31% 36% 9% 23%
9	SB	262	47% 31% 20%
10	SC	263	36% 37% 26%
11	SD	221	8% 41% 29% 29%
12	SE	189	51% 44%
13	SF	261	54% 41%
14	SG	272	51% 30% 18%
15	SH	306	37% 29% 33%
16	SI	195	9% 59% 31% 8%
17	SJ	194	13% 57% 37%
18	SK	130	63% 33%
19	SL	218	46% 29% 22%
20	SM	144	9% 51% 42%
21	SN	118	12% 42% 38% 17%
22	SO	137	7% 40% 16% 42%
23	SP	151	46% 35% 16%
24	SQ	145	69% 28%
25	SR	141	46% 52% 17% 30%
26	SS	156	33% 46% 18%
27	ST	54	13% 48% 41% 11%
28	SU	151	58% 39%

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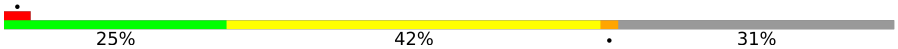
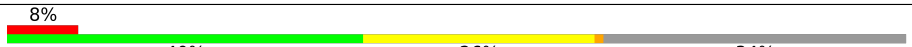
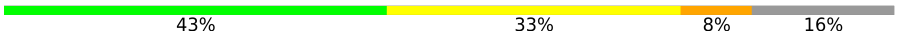
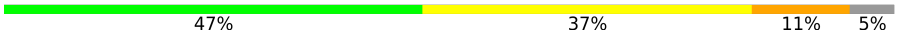
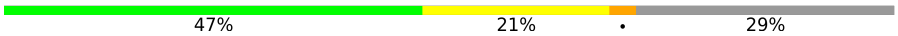
Mol	Chain	Length	Quality of chain
29	SV	161	
30	SW	137	
31	SX	145	
32	SY	170	
33	SZ	82	
34	AA	3788	
35	AC	159	
36	AB	119	
37	AL	215	
38	A1	146	
39	A2	127	
40	A4	67	
41	A6	108	
42	A7	120	
43	AN	165	
44	A8	131	
45	A9	140	
46	Aa	150	
47	Ab	112	
48	Ad	87	
49	Ae	51	
50	Af	128	
51	AP	205	
52	Ah	96	
53	Ai	104	

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Mol	Chain	Length	Quality of chain
54	AI	221	57% 32% 5% 6%
55	AJ	283	51% 25% 22%
56	Ac	92	59% 34%
57	AK	202	62% 35%
58	AM	139	64% 29% 5%
59	AS	187	78% 20%
60	AO	148	65% 34%
61	AQ	219	52% 31% 14%
62	AR	294	59% 25% 14%
63	AW	173	73% 25%
64	AY	190	32% 19% 47%
65	AT	182	73% 25%
66	AZ	126	60% 33%
67	A3	124	75% 20%
68	A5	257	57% 26% 13%
69	AD	260	66% 27% 5%
70	AE	386	74% 23%
71	AF	411	68% 25% 5%
72	AG	173	42% 29% 28%
73	AU	184	72% 24%
74	AH	190	67% 26%
75	AV	161	74% 22%
76	Ag	39	69% 26% 5%
77	AX	139	35% 31% 30%
78	A0	162	23% 15% 62%

2 Entry composition (i)

There are 78 unique types of molecules in this entry. The entry contains 192985 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	S1	120	985	632	189	162	2	0	0

- Molecule 2 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
2	S2	41	320	208	56	56	0	0

- Molecule 3 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	S3	95	781	478	169	128	6	0	0

- Molecule 4 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	S4	76	586	368	102	107	9	0	0

- Molecule 5 is a protein called 40S ribosomal protein S28e.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	S5	59	465	290	94	80	1	0	0

- Molecule 6 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
6	S6	43	345	213	75	57	0	0

- Molecule 7 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	S7	74	Total	C	N	O	P	0	0
			1571	702	275	521	73		

- Molecule 8 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	SA	1608	Total	C	N	O	P	0	0
			34208	15346	6106	11170	1586		

- Molecule 9 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	SB	210	Total	C	N	O	S	0	0
			1713	1097	301	303	12		

- Molecule 10 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	SC	195	Total	C	N	O	S	0	0
			1538	990	266	273	9		

- Molecule 11 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	SD	157	Total	C	N	O	S	0	0
			1228	782	225	214	7		

- Molecule 12 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	SE	185	Total	C	N	O	S	0	0
			1514	962	290	260	2		

- Molecule 13 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	SF	257	Total	C	N	O	S	0	0
			2061	1320	377	356	8		

- Molecule 14 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	SG	224	Total	C	N	O	S	0	0
			1757	1132	307	309	9		

- Molecule 15 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	SH	204	Total	C	N	O	S	0	0
			1651	1046	316	283	6		

- Molecule 16 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	SI	180	Total	C	N	O	S	0	0
			1424	893	263	258	10		

- Molecule 17 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	SJ	188	Total	C	N	O	S	0	0
			1528	982	264	278	4		

- Molecule 18 is a protein called 40S ribosomal protein S15A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	SK	129	Total	C	N	O	S	0	0
			1037	665	189	178	5		

- Molecule 19 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	SL	171	Total	C	N	O	S	0	0
			1383	872	264	243	4		

- Molecule 20 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	SM	138	Total	C	N	O	S	0	0
			1098	704	200	193	1		

- Molecule 21 is a protein called 40S ribosomal protein S20e.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	SN	98	Total	C	N	O	S	0	0
			772	484	135	148	5		

- Molecule 22 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	SO	79	Total	C	N	O	S	0	0
			686	450	116	118	2		

- Molecule 23 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	SP	127	Total	C	N	O	S	0	0
			954	591	184	176	3		

- Molecule 24 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	SQ	144	Total	C	N	O	S	0	0
			1129	712	222	193	2		

- Molecule 25 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	SR	98	Total	C	N	O	S	0	0
			746	474	123	145	4		

- Molecule 26 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	SS	128	Total	C	N	O	S	0	0
			1046	657	205	180	4		

- Molecule 27 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	ST	48	Total	C	N	O	S	0	0
			405	252	85	64	4		

- Molecule 28 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	SU	149	Total	C	N	O	S	0	0
			1202	769	220	210	3		

- Molecule 29 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	SV	146	Total	C	N	O	S	0	0
			1206	772	227	200	7		

- Molecule 30 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	SW	95	Total	C	N	O	S	0	0
			785	498	149	135	3		

- Molecule 31 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	SX	96	Total	C	N	O	S	0	0
			776	497	137	138	4		

- Molecule 32 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	SY	154	Total	C	N	O	S	0	0
			1266	811	239	214	2		

- Molecule 33 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	SZ	72	Total	C	N	O	S	0	0
			557	346	102	105	4		

- Molecule 34 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	AA	3193	Total	C	N	O	P	0	0
			67884	30446	12053	22224	3161		

- Molecule 35 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	AC	151	Total	C	N	O	P	0	0
			3215	1444	589	1034	148		

- Molecule 36 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	AB	118	Total	C	N	O	P	0	0
			2517	1126	457	817	117		

- Molecule 37 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	AL	211	Total	C	N	O	S	0	0
			1761	1119	349	290	3		

- Molecule 38 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	A1	140	Total	C	N	O	S	0	0
			1134	736	204	191	3		

- Molecule 39 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	A2	105	Total	C	N	O	S	0	0
			837	534	152	148	3		

- Molecule 40 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	A4	66	Total	C	N	O	S	0	0
			555	347	116	90	2		

- Molecule 41 is a protein called 60S ribosomal protein L30e.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	A6	98	Total	C	N	O	S	0	0
			740	462	132	139	7		

- Molecule 42 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	A7	96	Total 793	C 508	N 151	O 129	S 5	0	0

- Molecule 43 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	AN	147	Total 1210	C 787	N 212	O 205	S 6	0	0

- Molecule 44 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	A8	125	Total 1036	C 660	N 206	O 163	S 7	0	0

- Molecule 45 is a protein called 60S ribosomal protein L35ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	A9	103	Total 844	C 543	N 163	O 135	S 3	0	0

- Molecule 46 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Aa	106	Total 850	C 523	N 184	O 137	S 6	0	0

- Molecule 47 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	Ab	95	Total 756	C 477	N 150	O 129	0	0

- Molecule 48 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Ad	72	Total 603	C 395	N 107	O 99	S 2	0	0

- Molecule 49 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Ae	43	Total	C	N	O	S	0	0
			388	243	92	52	1		

- Molecule 50 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Af	51	Total	C	N	O	S	0	0
			413	255	87	66	5		

- Molecule 51 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	AP	204	Total	C	N	O	S	0	0
			1697	1075	351	267	4		

- Molecule 52 is a protein called Large ribosomal subunit protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Ah	85	Total	C	N	O	S	0	0
			658	417	127	107	7		

- Molecule 53 is a protein called Large ribosomal subunit protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	Ai	95	Total	C	N	O	S	0	0
			778	490	152	127	9		

- Molecule 54 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	AI	207	Total	C	N	O	S	0	0
			1685	1096	298	286	5		

- Molecule 55 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	AJ	222	Total	C	N	O	S	0	0
			1813	1174	323	309	7		

- Molecule 56 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	Ac	89	Total	C	N	O	S	0	0
			709	441	150	113	5		

- Molecule 57 is a protein called 60S ribosomal protein L13, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	AK	201	Total	C	N	O	S	0	0
			1659	1064	311	276	8		

- Molecule 58 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	AM	132	Total	C	N	O	S	0	0
			996	631	179	178	8		

- Molecule 59 is a protein called 60S ribosomal protein L18-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	AS	186	Total	C	N	O	S	0	0
			1503	958	299	241	5		

- Molecule 60 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	AO	147	Total	C	N	O	S	0	0
			1172	747	232	189	4		

- Molecule 61 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	AQ	189	Total	C	N	O	S	0	0
			1544	984	291	261	8		

- Molecule 62 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	AR	252	Total	C	N	O	S	0	0
			2049	1301	385	357	6		

- Molecule 63 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	AW	170	Total	C	N	O	S	0	0
			1319	824	266	222	7		

- Molecule 64 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	AY	101	Total	C	N	O	S	0	0
			796	502	144	144	6		

- Molecule 65 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	AT	181	Total	C	N	O	S	0	0
			1509	952	309	244	4		

- Molecule 66 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	AZ	121	Total	C	N	O	S	0	0
			1000	626	206	165	3		

- Molecule 67 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	A3	119	Total	C	N	O	S	0	0
			994	635	194	163	2		

- Molecule 68 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	A5	223	Total	C	N	O	S	0	0
			1879	1211	357	306	5		

- Molecule 69 is a protein called 60S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	AD	247	Total	C	N	O	S	0	0
			1866	1166	374	317	9		

- Molecule 70 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	AE	380	Total	C	N	O	S	0	0
			3061	1948	575	521	17		

- Molecule 71 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	AF	390	Total	C	N	O	S	0	0
			3094	1962	594	527	11		

- Molecule 72 is a protein called 60S ribosomal protein L11a.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	AG	124	Total	C	N	O	S	0	0
			1010	636	197	171	6		

- Molecule 73 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	AU	180	Total	C	N	O	S	0	0
			1497	946	289	255	7		

- Molecule 74 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	AH	185	Total	C	N	O	S	0	0
			1475	950	264	255	6		

- Molecule 75 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	AV	155	Total	C	N	O	S	0	0
			1275	814	241	214	6		

- Molecule 76 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Ag	37	Total	C	N	O	S	0	0
			343	210	86	45	2		

- Molecule 77 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	AX	97	Total	C	N	O	S	0	0
			824	548	135	139	2		

- Molecule 78 is a protein called 60S ribosomal protein L24.

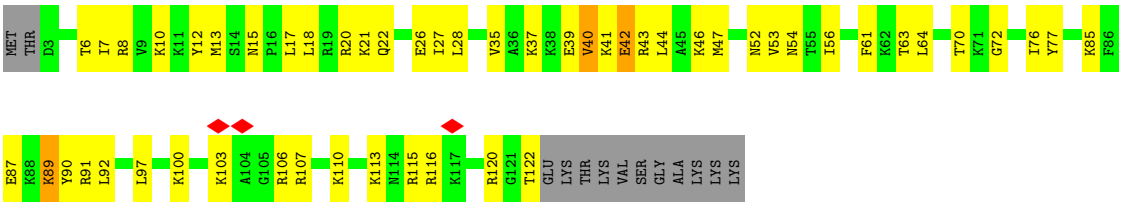
Mol	Chain	Residues	Atoms					AltConf	Trace
78	A0	62	Total	C	N	O	S	0	0
			521	336	97	87	1		

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

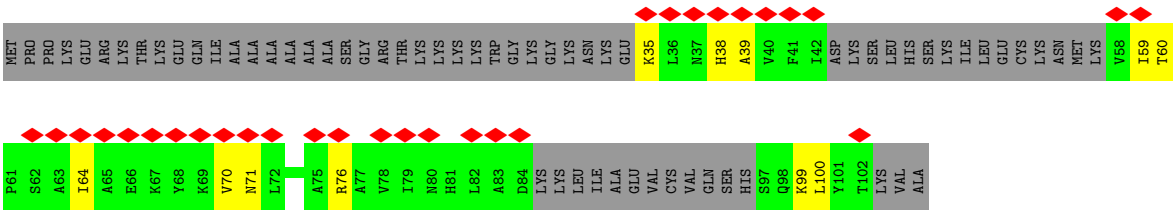
• Molecule 1: 40S ribosomal protein S24

Chain S1:



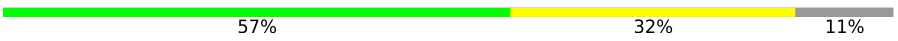
• Molecule 2: 40S ribosomal protein S25

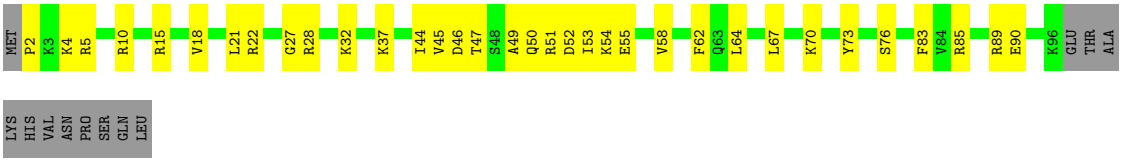
Chain S2:



• Molecule 3: 40S ribosomal protein S26

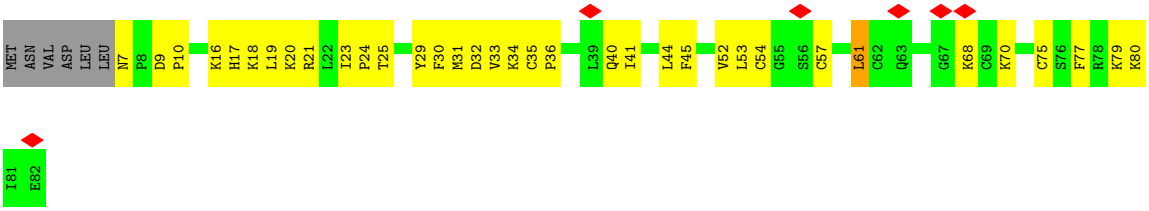
Chain S3:





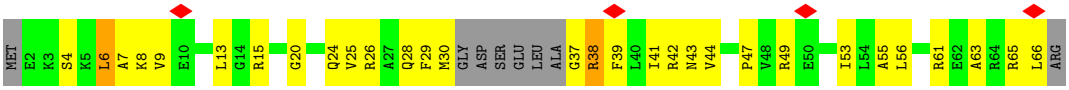
• Molecule 4: 40S ribosomal protein S27

Chain S4:



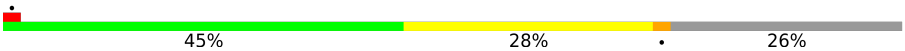
• Molecule 5: 40S ribosomal protein S28e

Chain S5:



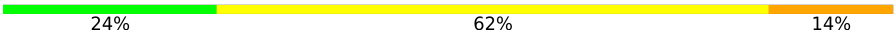
• Molecule 6: 40S ribosomal protein S30

Chain S6:



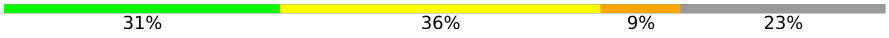
• Molecule 7: E-site tRNA

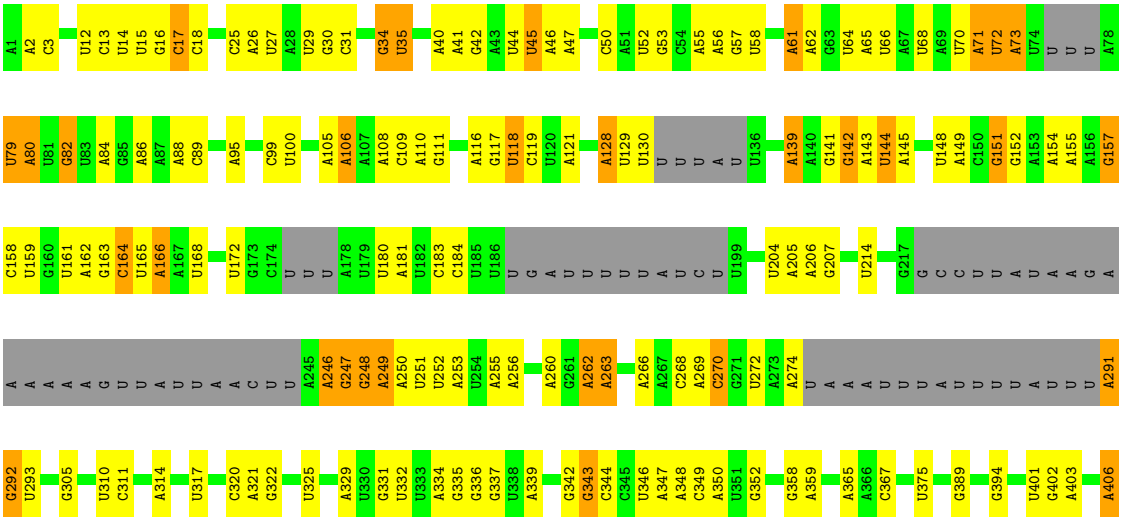
Chain S7:

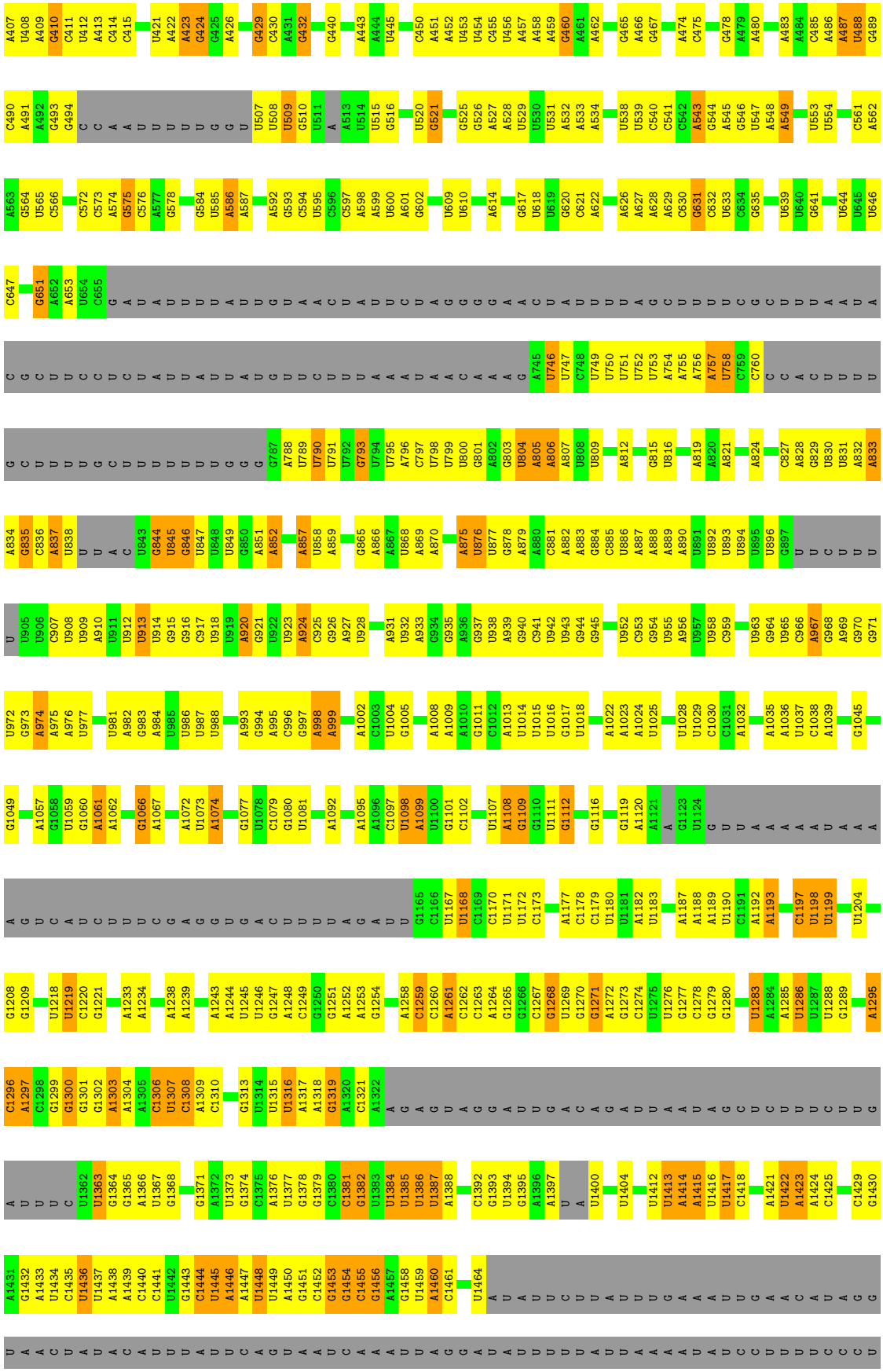


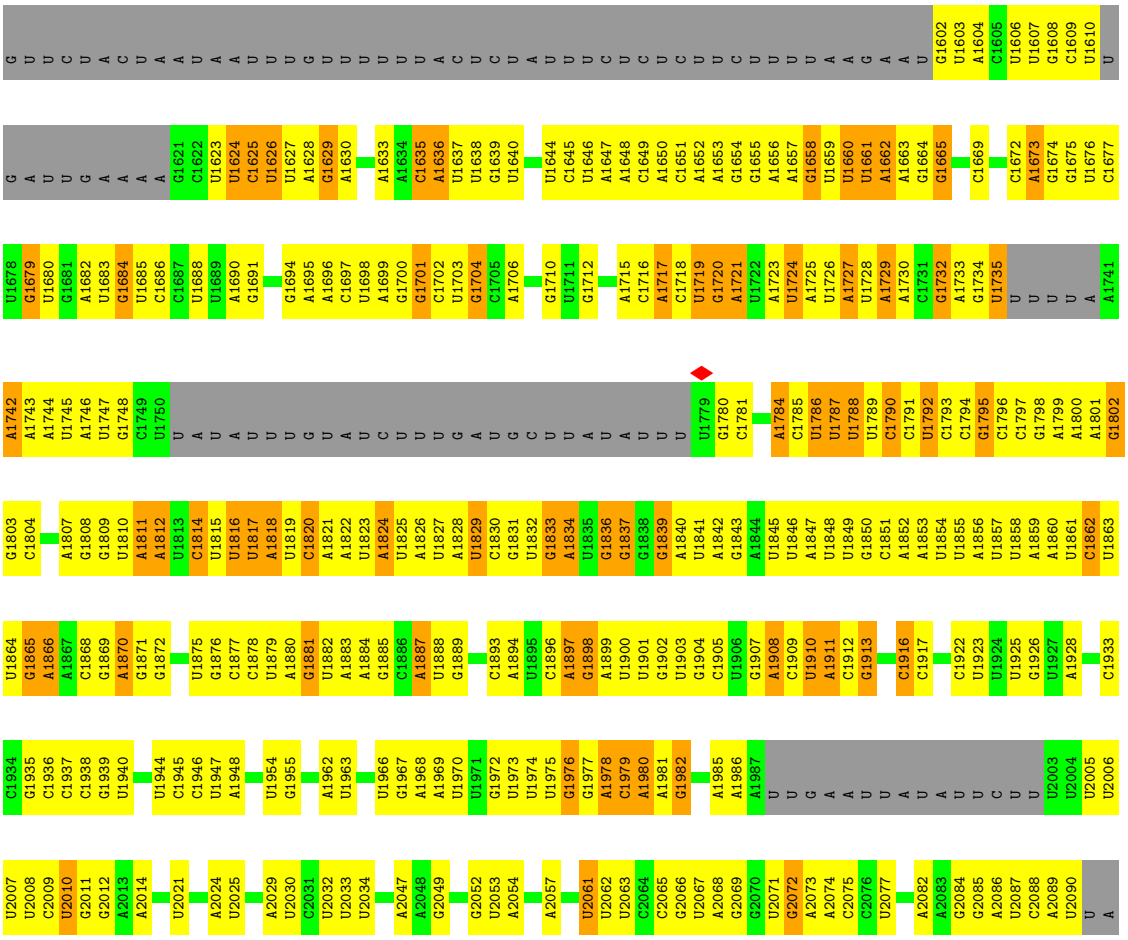
• Molecule 8: 18S ribosomal RNA

Chain SA:



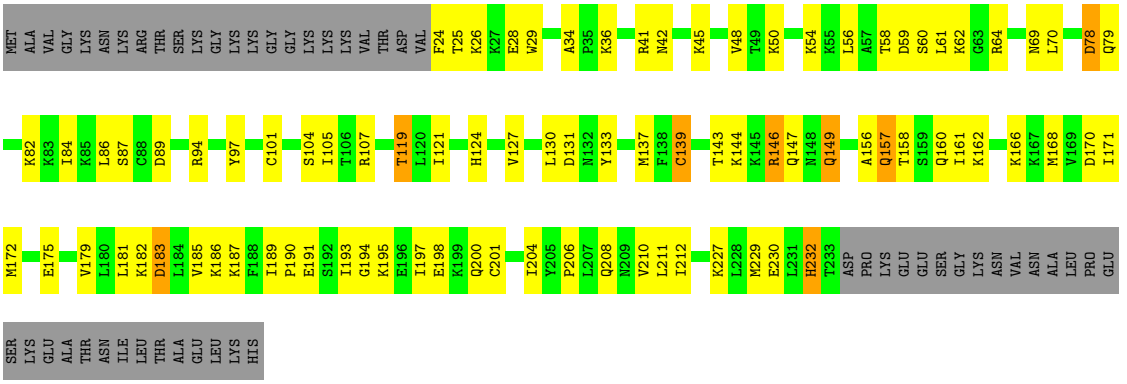






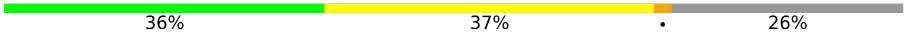
• Molecule 9: 40S ribosomal protein S3a

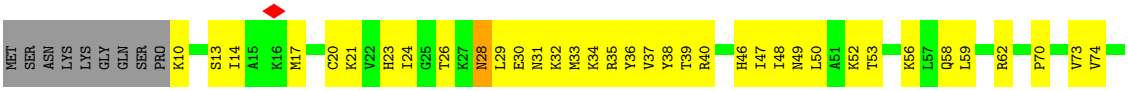
Chain SB:

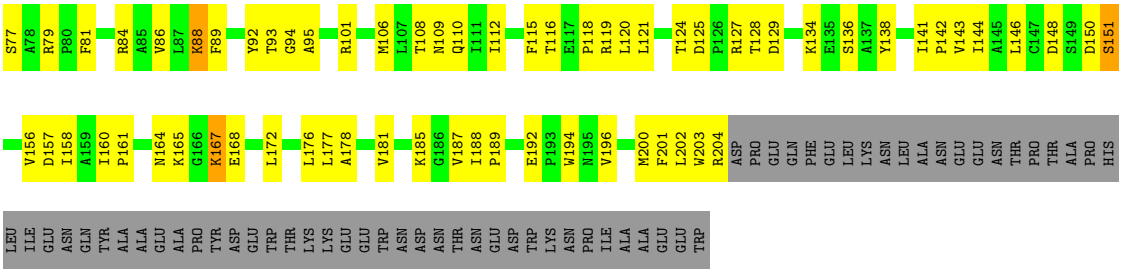


• Molecule 10: 40S ribosomal protein SA

Chain SC:

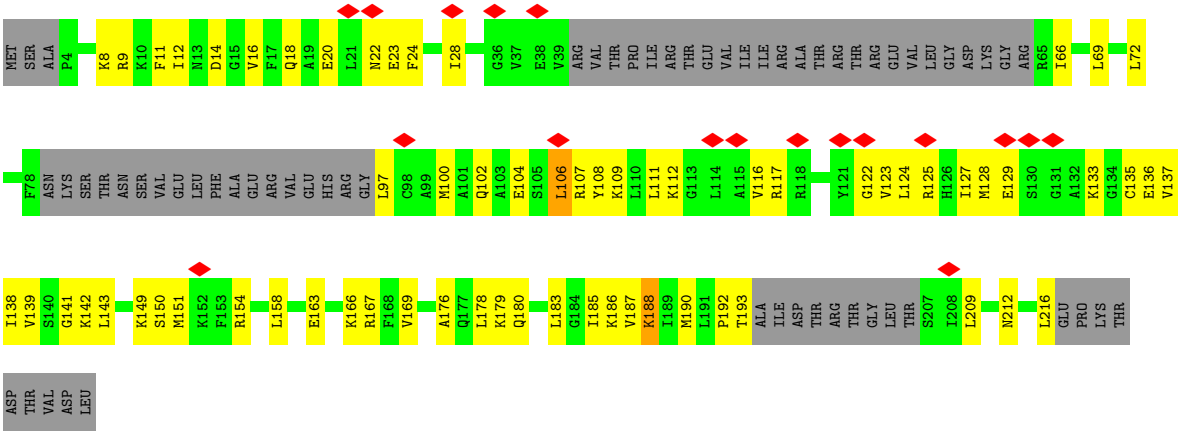






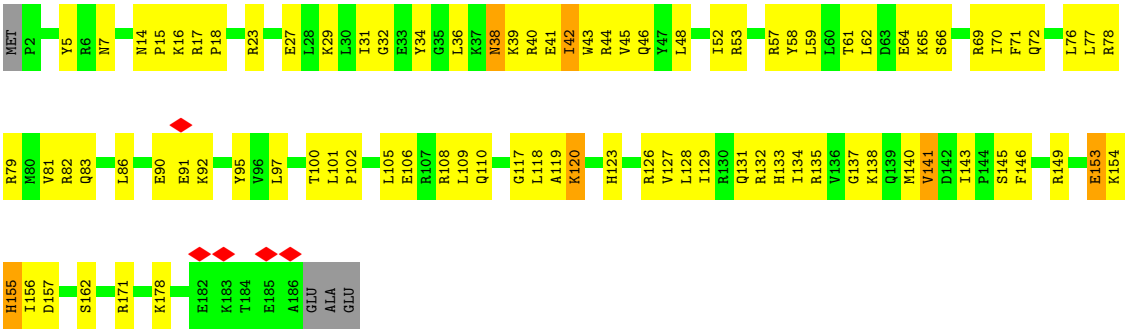
• Molecule 11: 40S ribosomal protein S3

Chain SD:



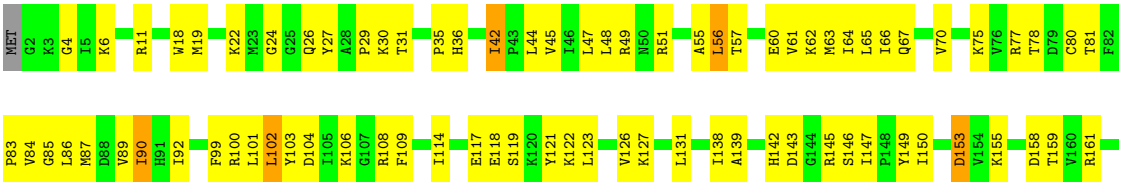
• Molecule 12: 40S ribosomal protein S9

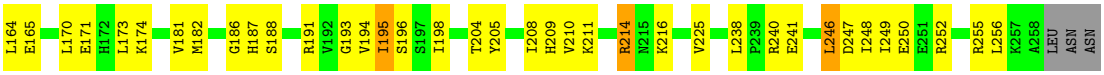
Chain SE:



• Molecule 13: 40S ribosomal protein S4

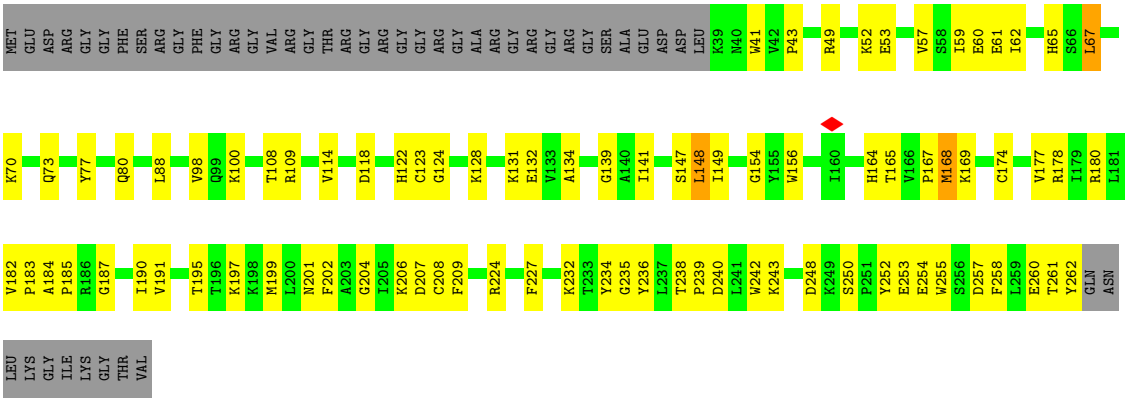
Chain SF:





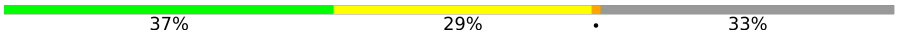
• Molecule 14: 40S ribosomal protein S5

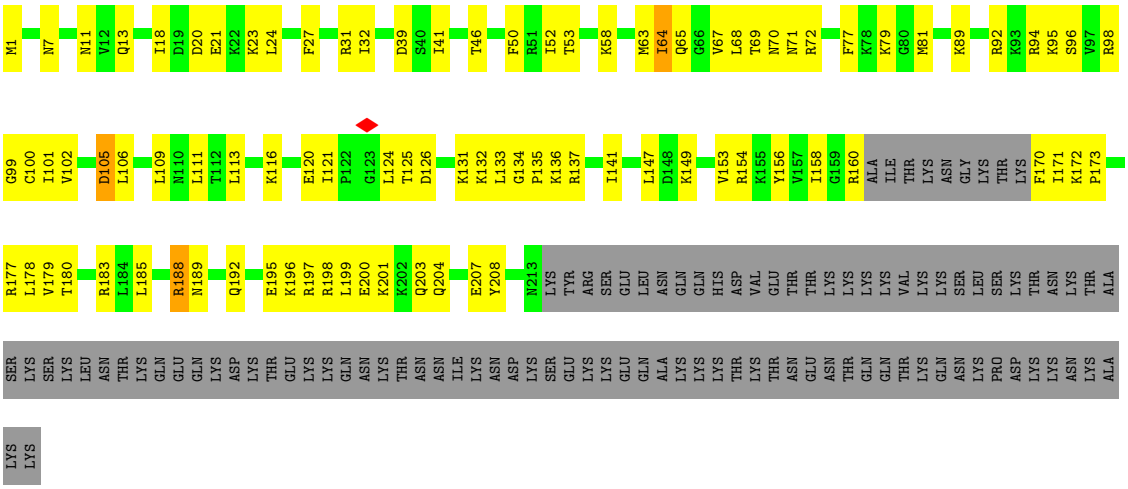
Chain SG:



• Molecule 15: 40S ribosomal protein S6

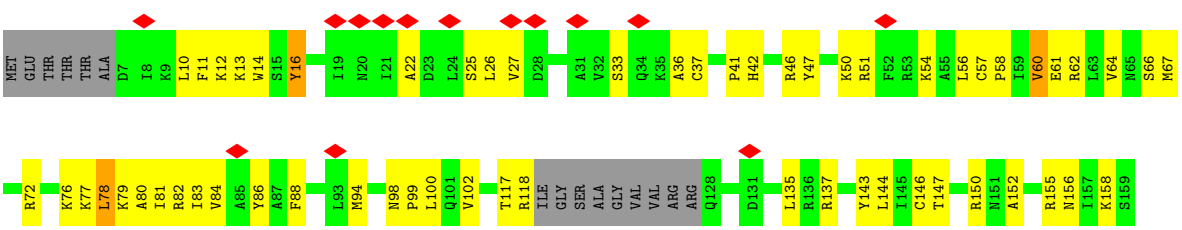
Chain SH:

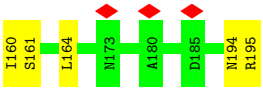




• Molecule 16: 40S ribosomal protein S5

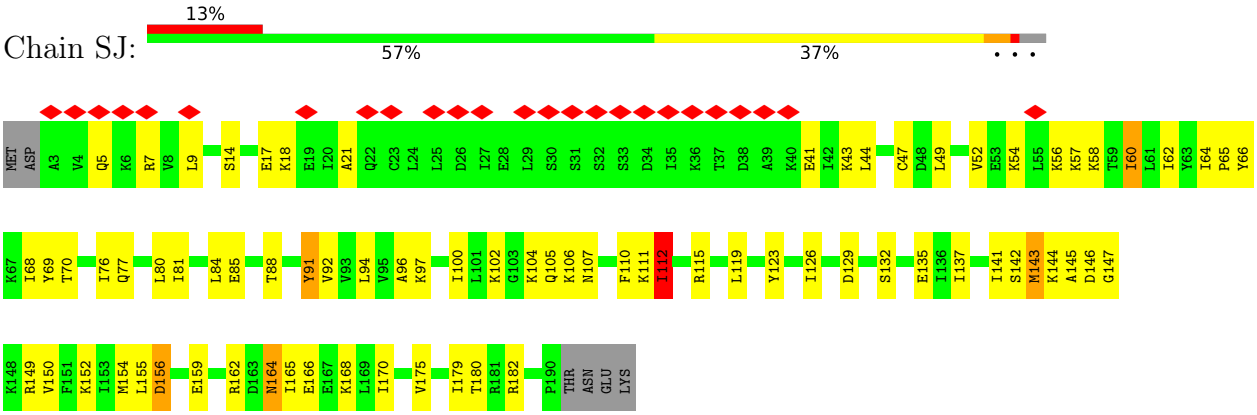
Chain SI:





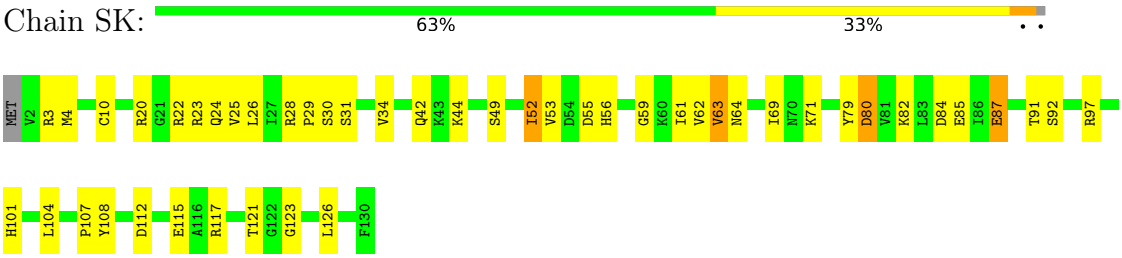
• Molecule 17: 40S ribosomal protein S7

Chain SJ:



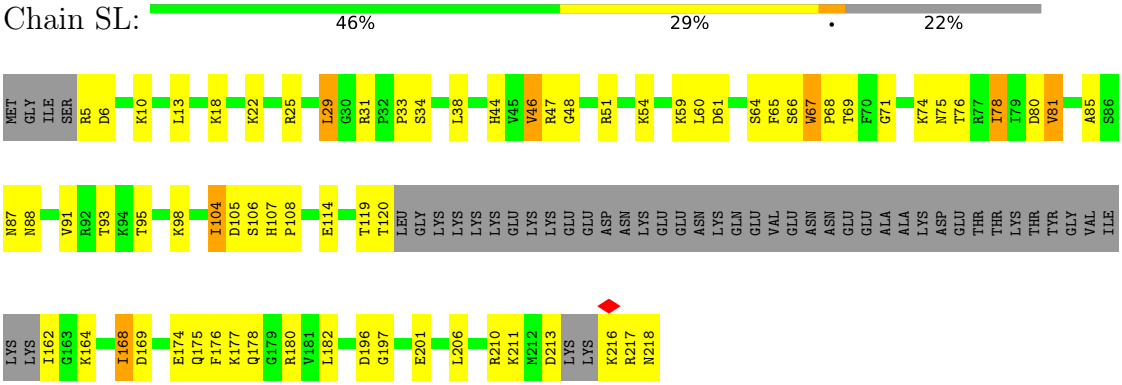
• Molecule 18: 40S ribosomal protein S15A

Chain SK:



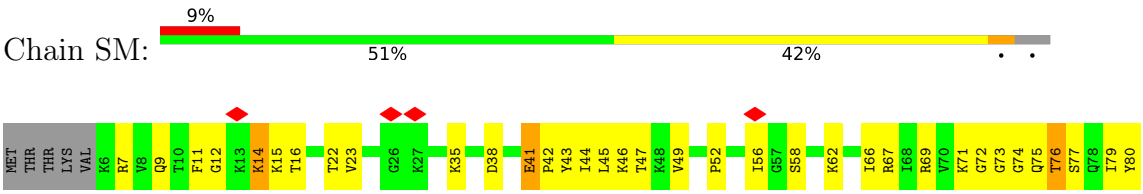
• Molecule 19: 40S ribosomal protein S8

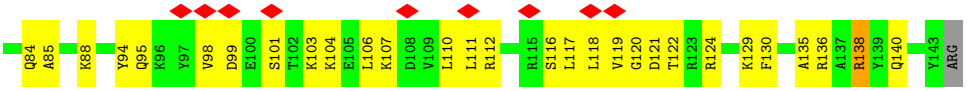
Chain SL:



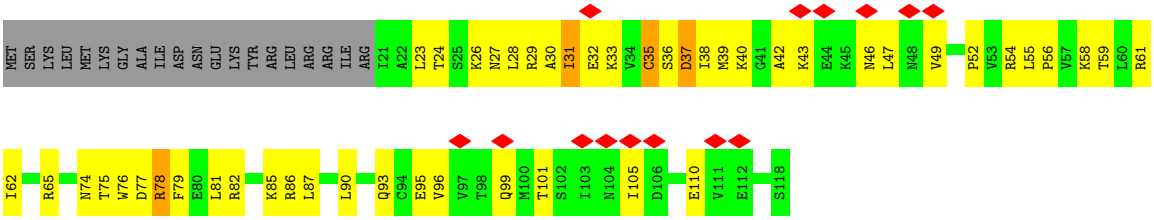
• Molecule 20: 40S ribosomal protein S16

Chain SM:

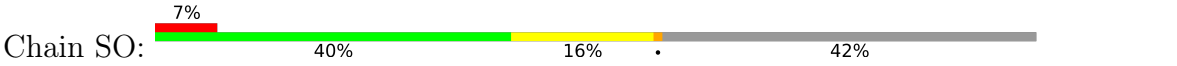


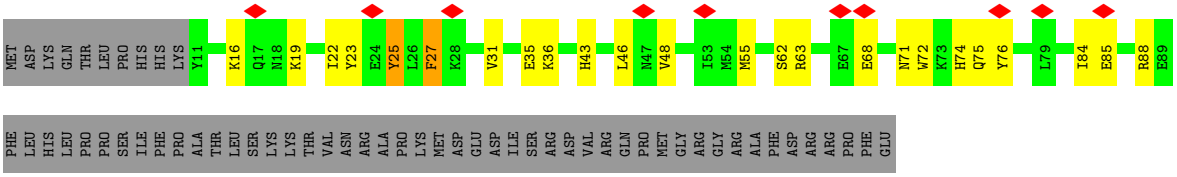


• Molecule 21: 40S ribosomal protein S20e

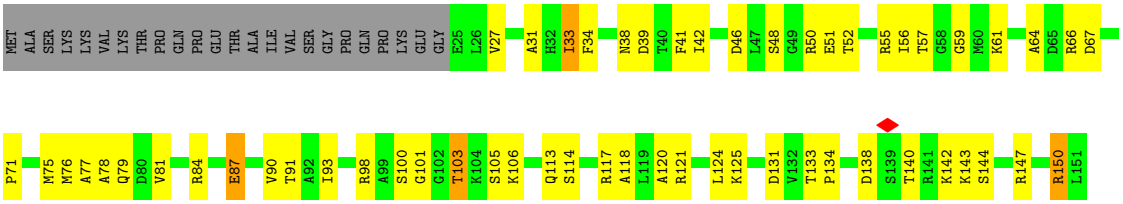


• Molecule 22: 40S ribosomal protein S10

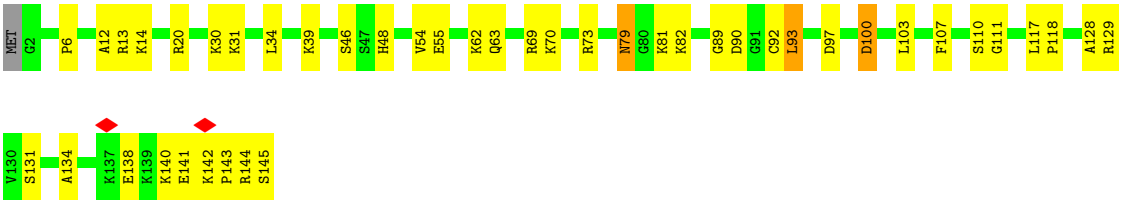




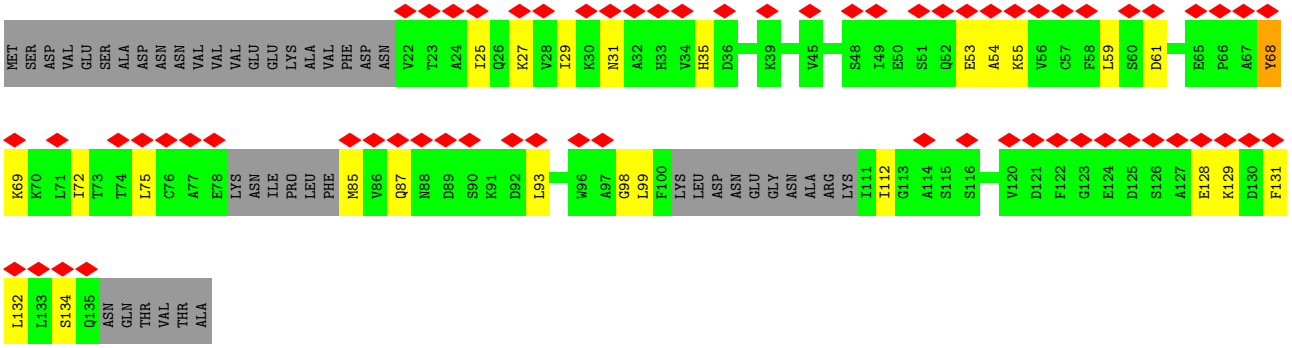
• Molecule 23: 40S ribosomal protein S11



• Molecule 24: 40S ribosomal protein S23

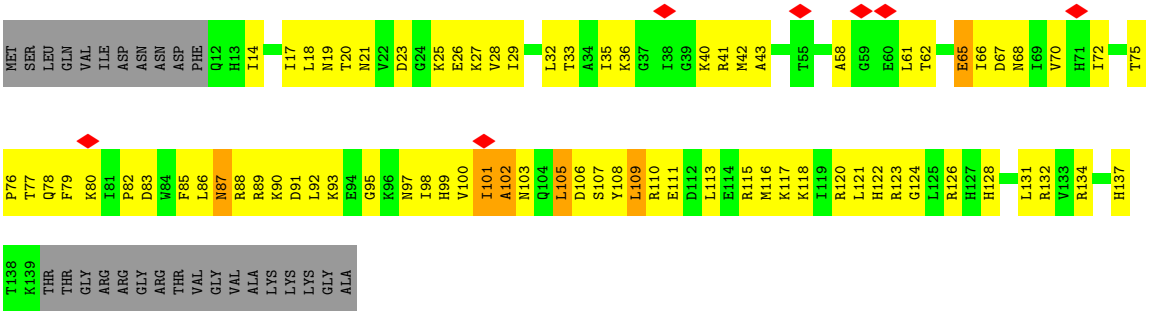


• Molecule 25: 40S ribosomal protein S12



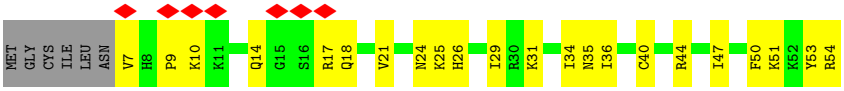
• Molecule 26: 40S ribosomal protein S18

Chain SS:



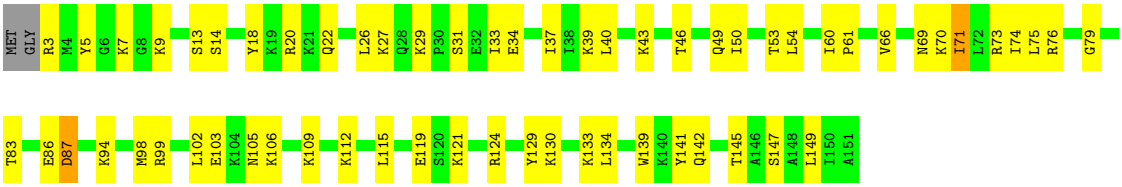
• Molecule 27: 40S ribosomal protein S29

Chain ST:



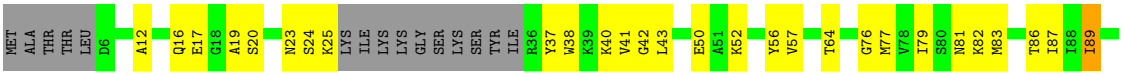
• Molecule 28: 40S ribosomal protein S15

Chain SU:



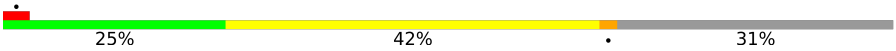
• Molecule 29: 40S ribosomal protein S11

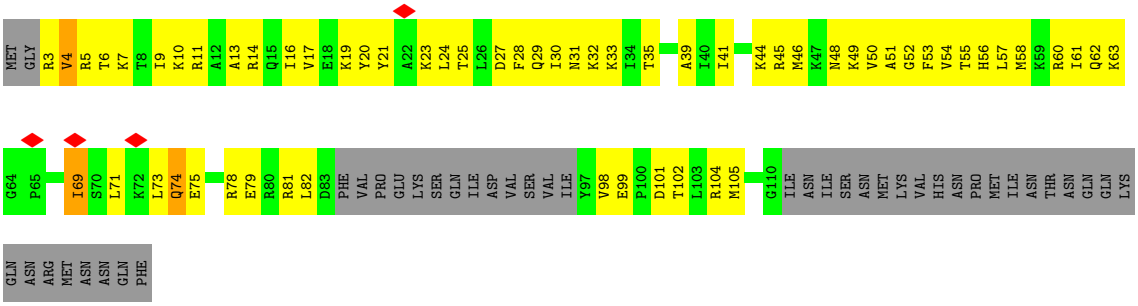
Chain SV:



• Molecule 30: 40S ribosomal protein S17

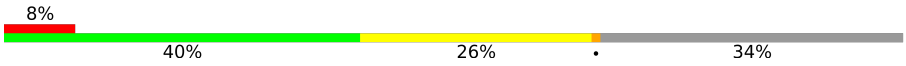
Chain SW:

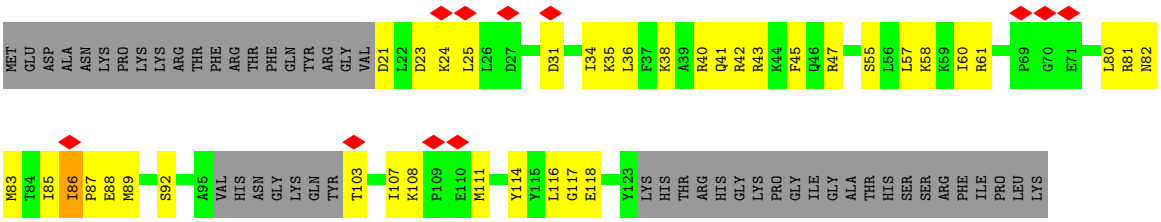




• Molecule 31: 40S ribosomal protein S19

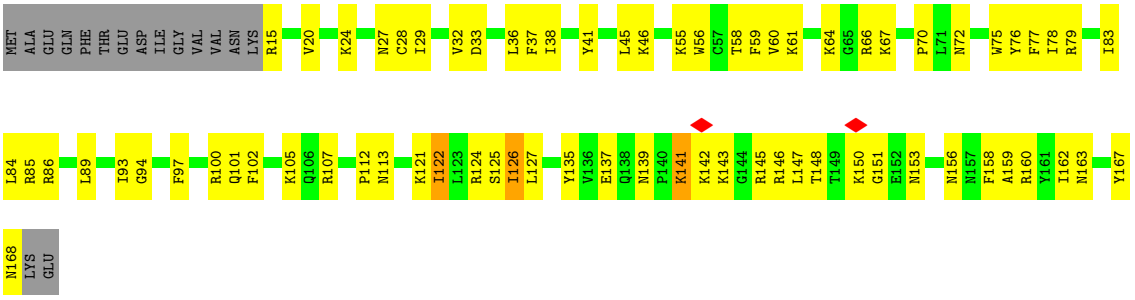
Chain SX:





• Molecule 32: 40S ribosomal protein S19

Chain SY:

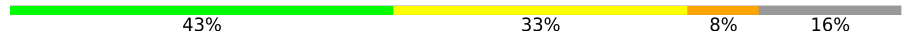


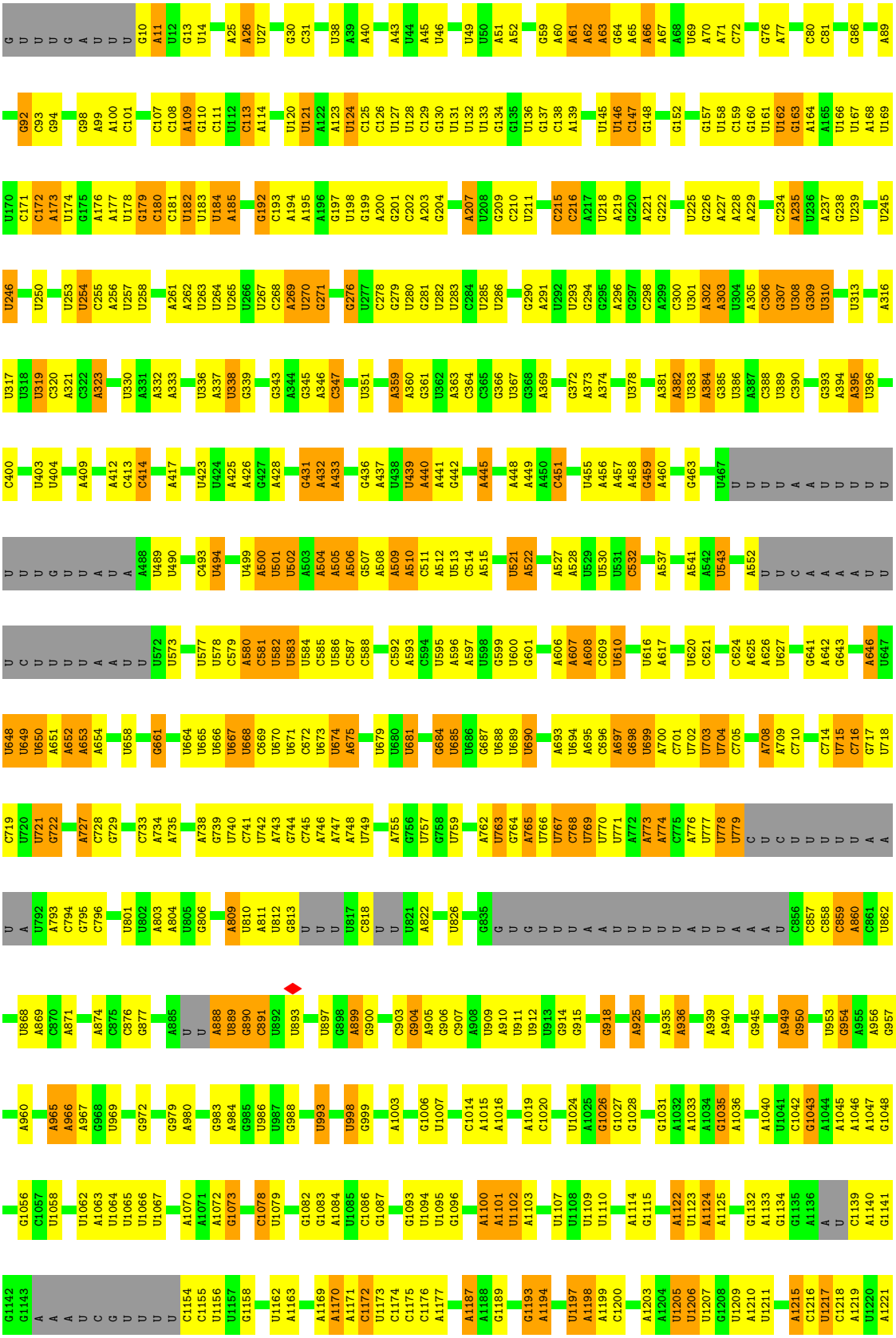
• Molecule 33: 40S ribosomal protein S21

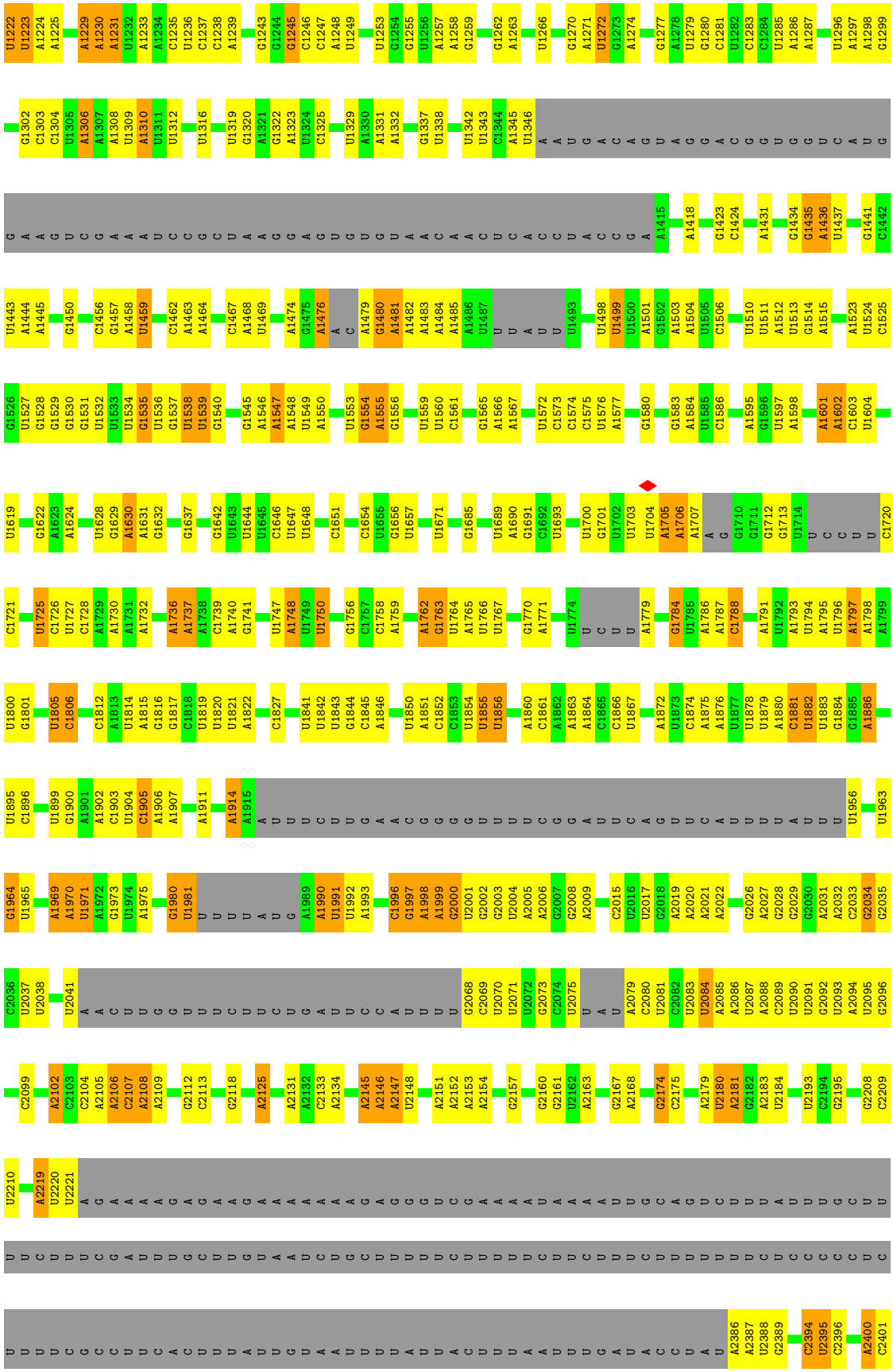
Chain SZ:

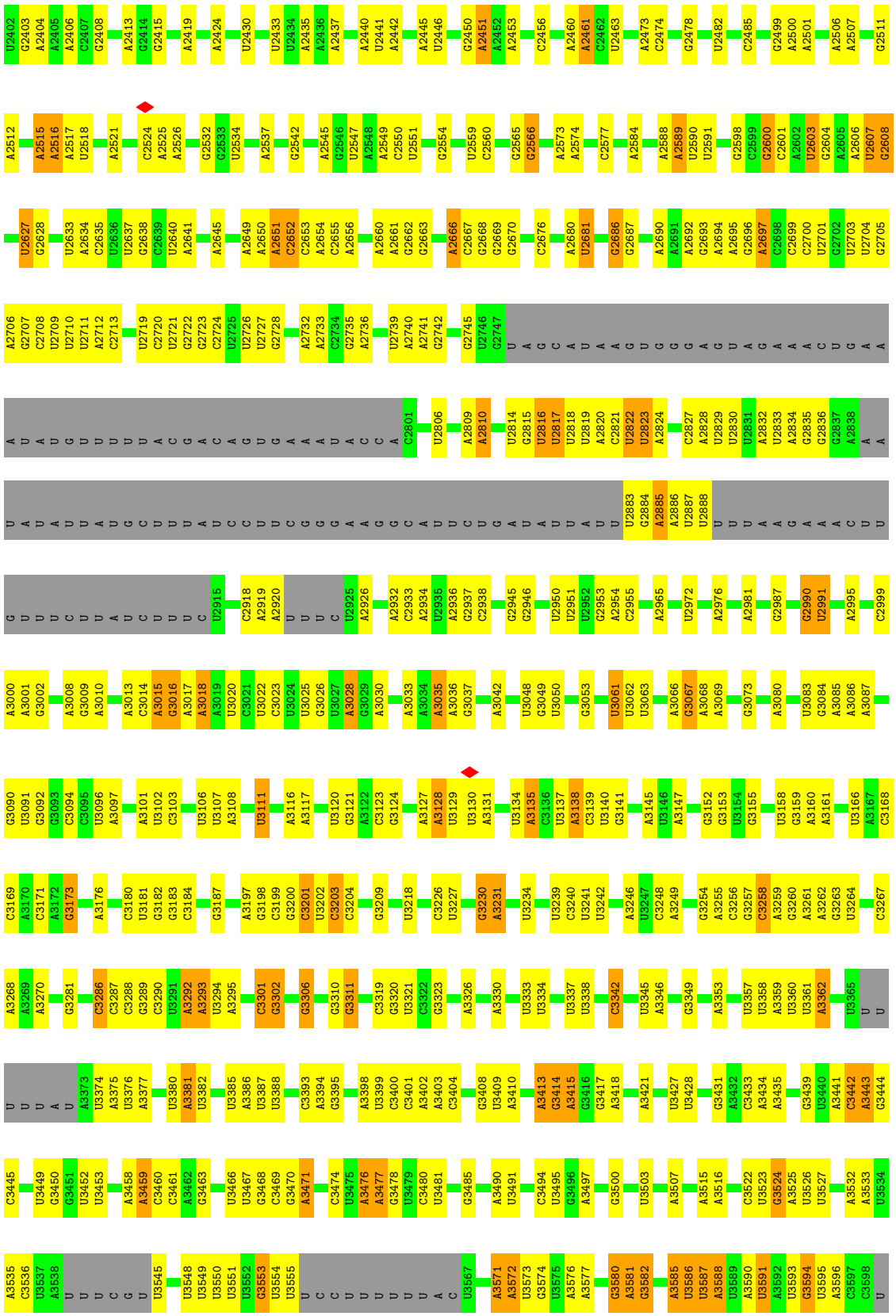
• Molecule 34: 28S ribosomal RNA

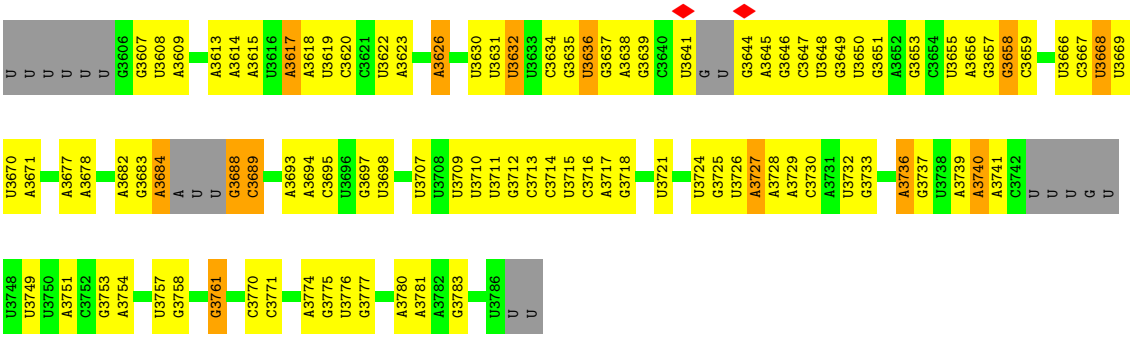
Chain AA:





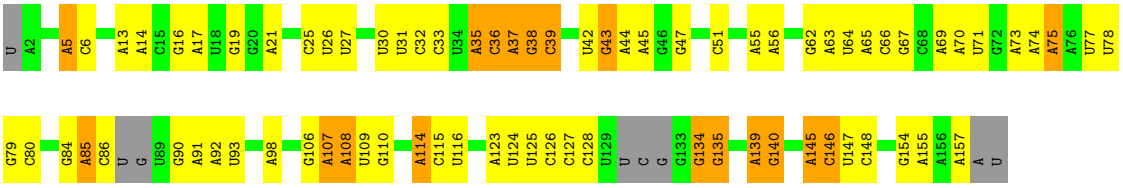






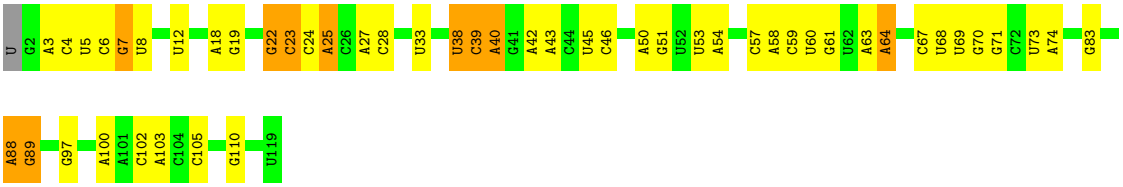
• Molecule 35: 5.8S ribosomal RNA

Chain AC:



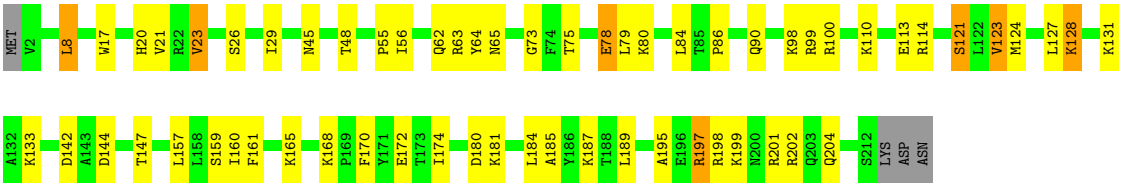
• Molecule 36: 5S ribosomal RNA

Chain AB:



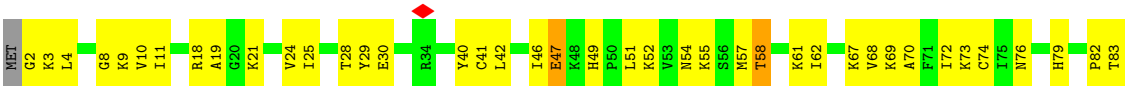
• Molecule 37: 60S ribosomal protein L13

Chain AL:



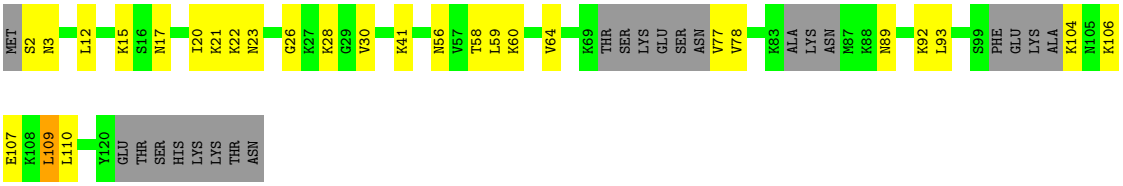
• Molecule 38: 60S ribosomal protein L27

Chain A1:



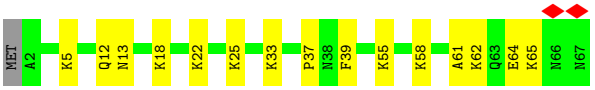
• Molecule 39: 60S ribosomal protein L28

Chain A2:



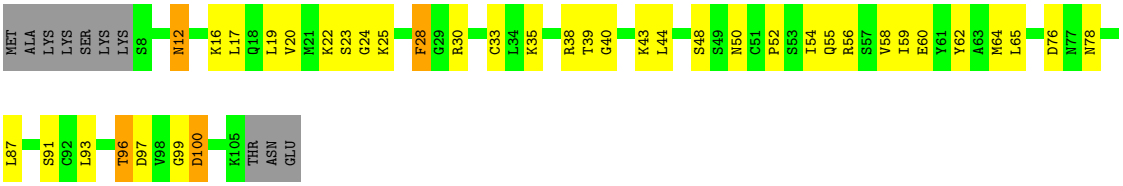
• Molecule 40: 60S ribosomal protein L29

Chain A4:



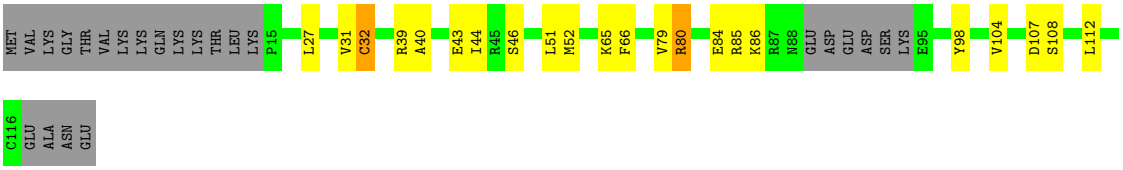
• Molecule 41: 60S ribosomal protein L30e

Chain A6:



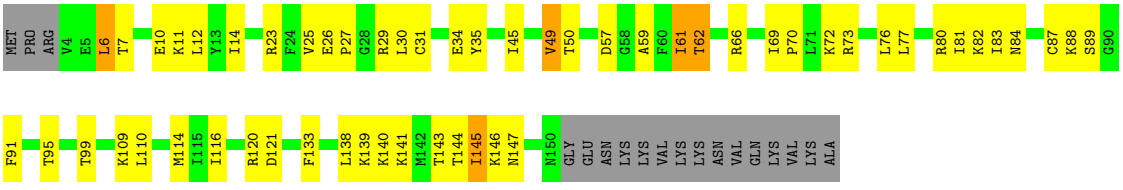
• Molecule 42: 60S ribosomal protein L31

Chain A7:



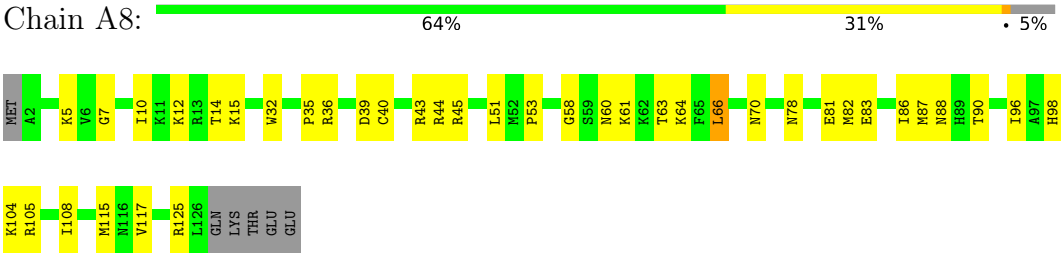
• Molecule 43: 60S ribosomal protein L14

Chain AN:



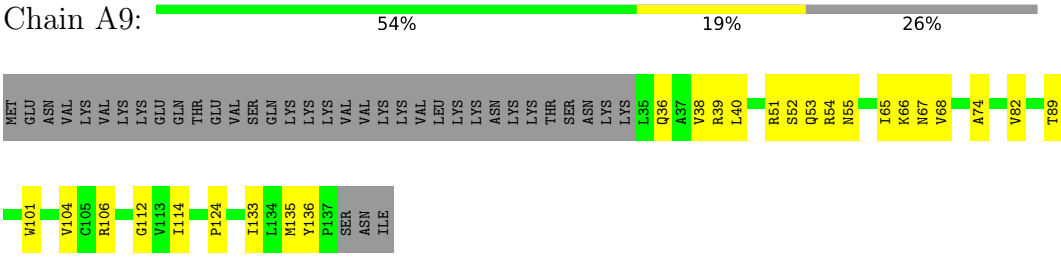
• Molecule 44: 60S ribosomal protein L32

Chain A8:



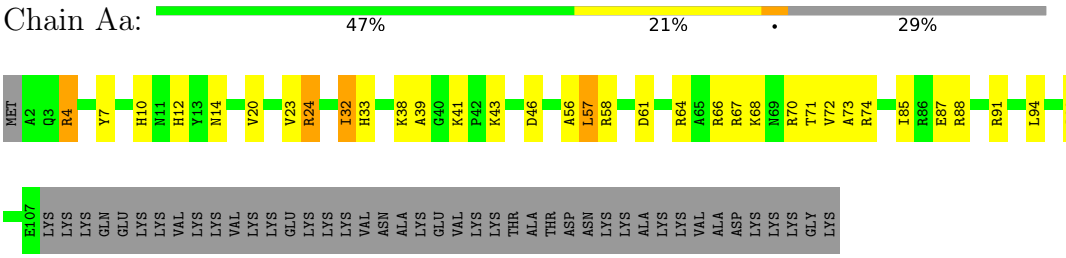
• Molecule 45: 60S ribosomal protein L35ae

Chain A9:



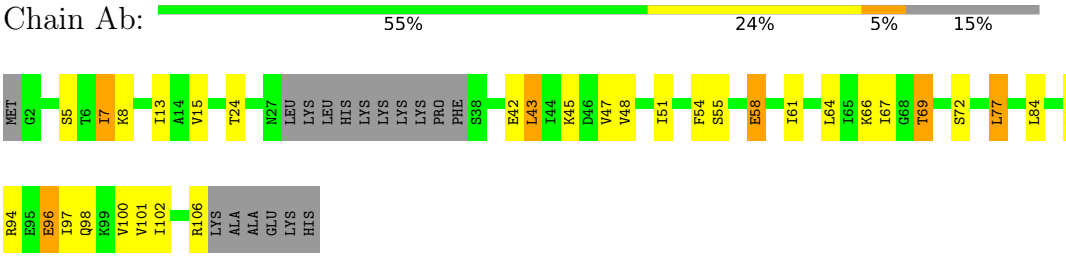
• Molecule 46: 60S ribosomal protein L34

Chain Aa:



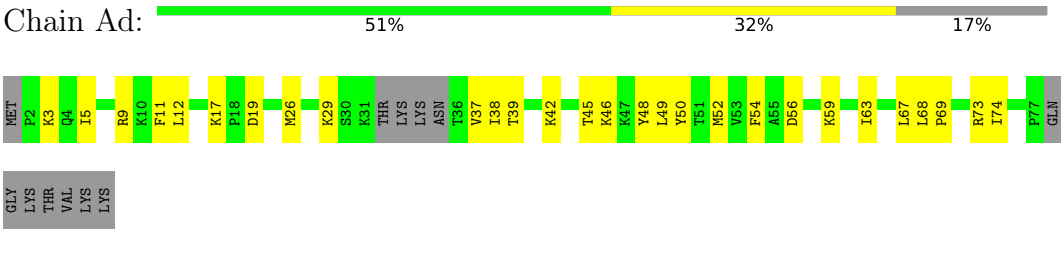
• Molecule 47: 60S ribosomal protein L36

Chain Ab:



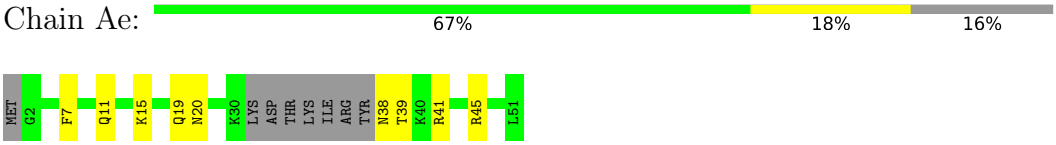
• Molecule 48: 60S ribosomal protein L38

Chain Ad:



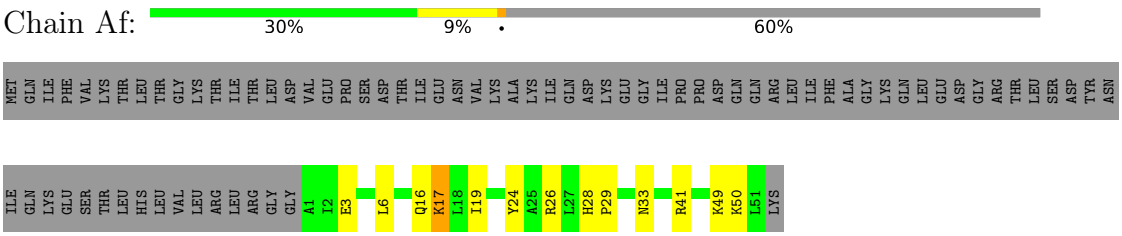
• Molecule 49: 60S ribosomal protein L39

Chain Ae:



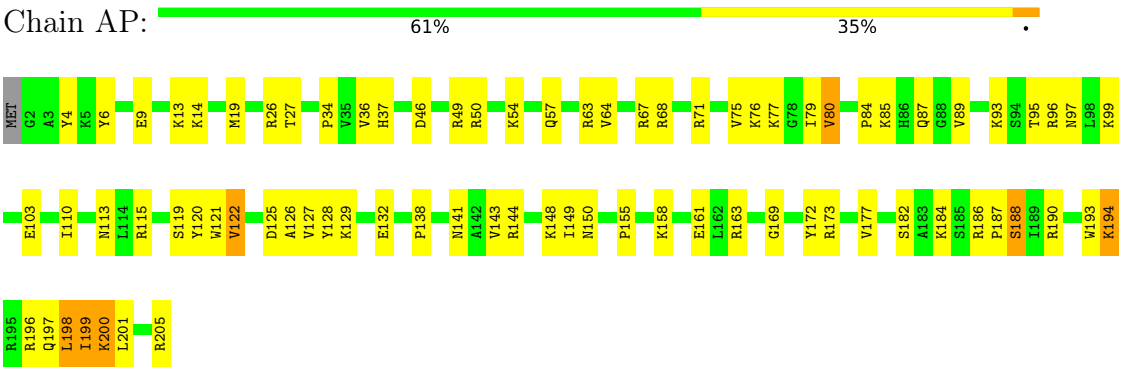
• Molecule 50: Ubiquitin-60S ribosomal protein L40

Chain Af:



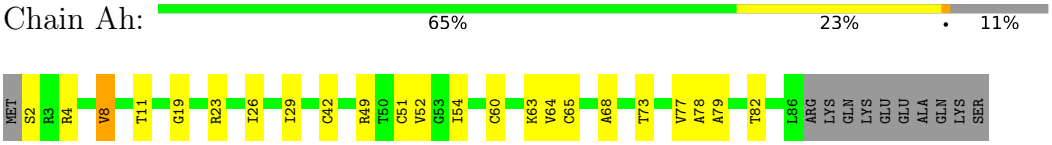
• Molecule 51: Ribosomal protein L15

Chain AP:



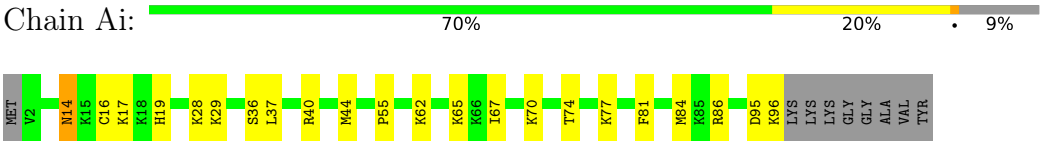
• Molecule 52: Large ribosomal subunit protein eL43

Chain Ah:



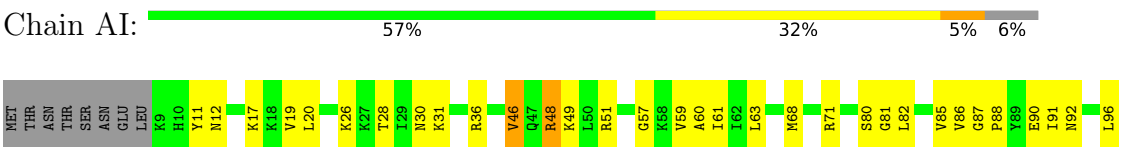
• Molecule 53: Large ribosomal subunit protein eL42

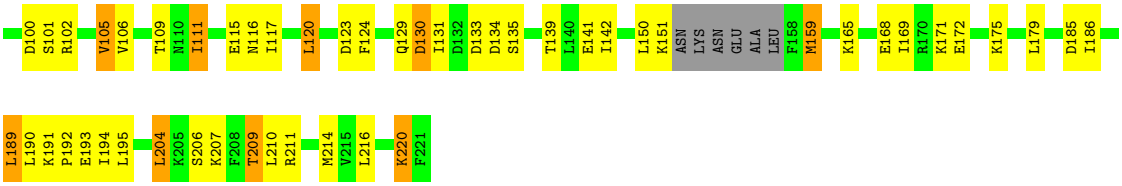
Chain Ai:



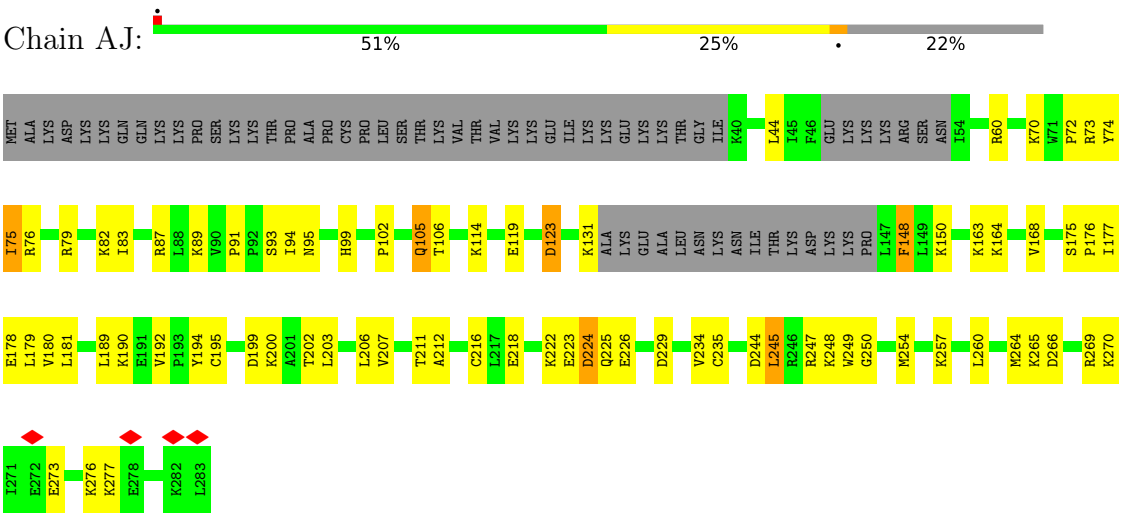
• Molecule 54: 60S ribosomal protein L6

Chain AI:

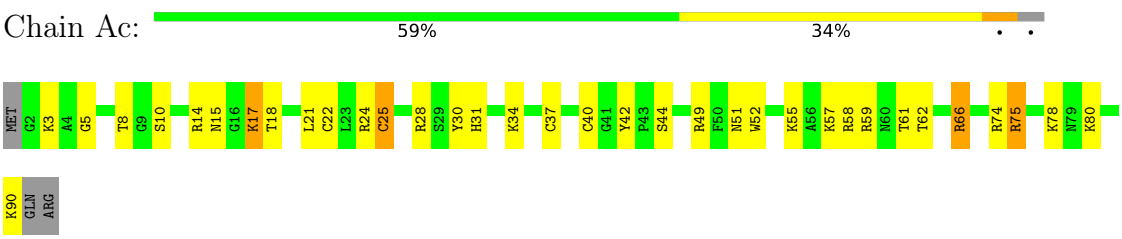




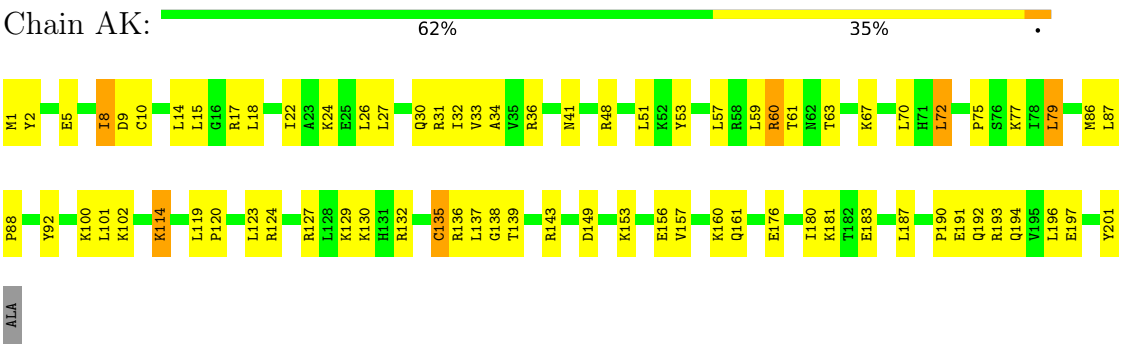
• Molecule 55: 60S ribosomal protein L7a



• Molecule 56: Ribosomal protein L37



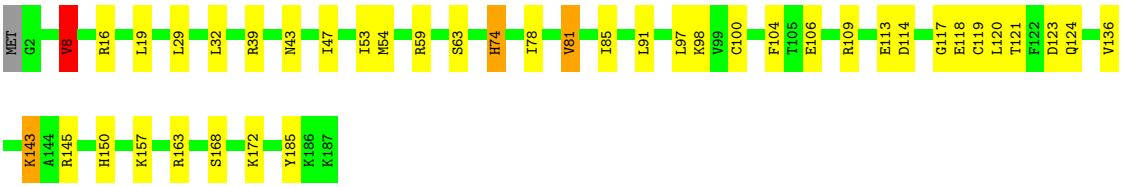
• Molecule 57: 60S ribosomal protein L13, putative



• Molecule 58: 60S ribosomal protein L23

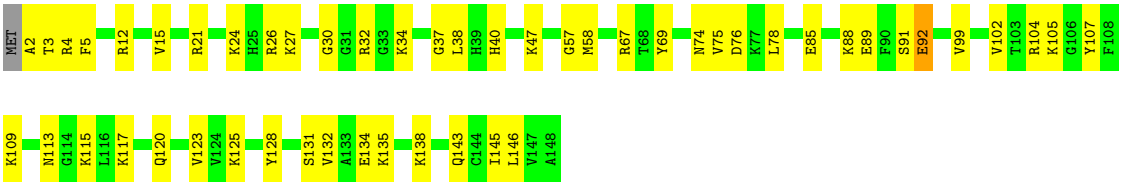
• Molecule 59: 60S ribosomal protein L18-2

Chain AS:



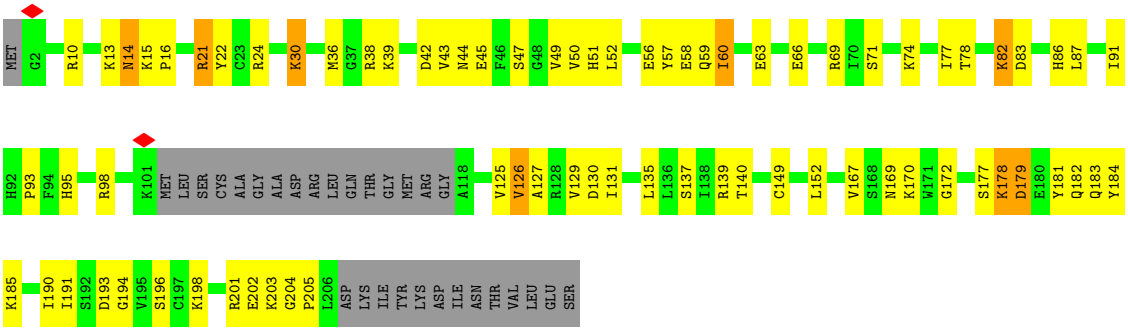
• Molecule 60: 60S ribosomal protein L27a

Chain AO:



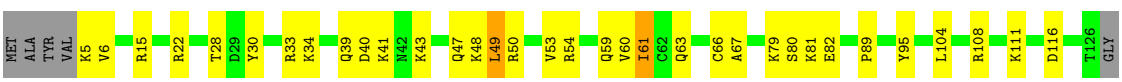
• Molecule 61: 60S ribosomal protein L10

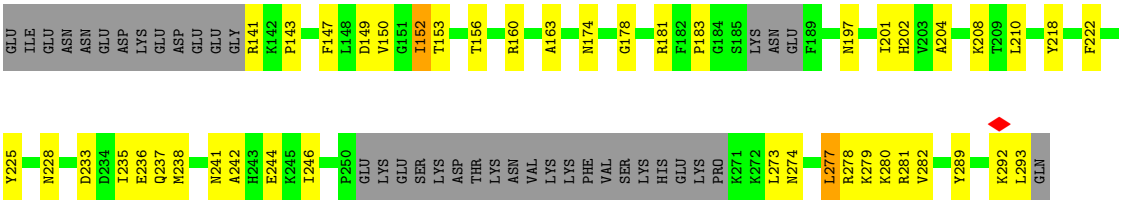
Chain AQ:



• Molecule 62: 60S ribosomal protein L5

Chain AR:



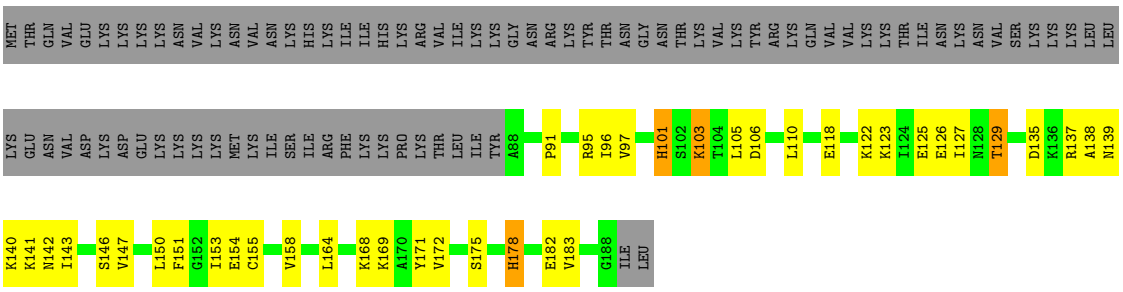


• Molecule 63: 60S ribosomal protein L17

Chain AW:

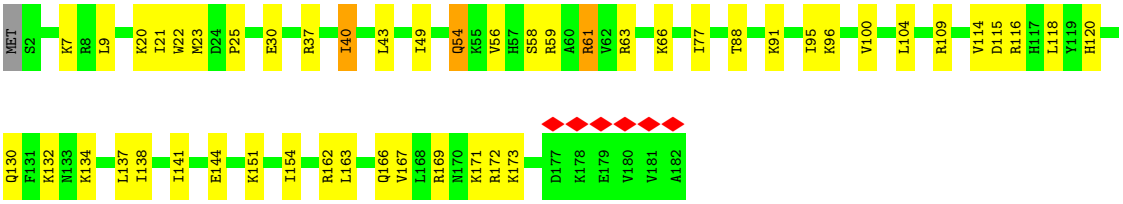
• Molecule 64: 60S ribosomal protein L23

Chain AY:



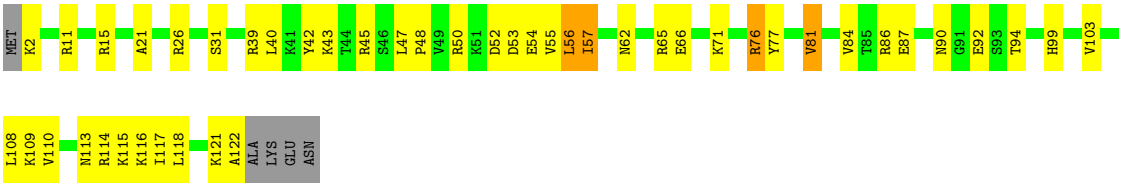
• Molecule 65: 60S ribosomal protein L19

Chain AT:



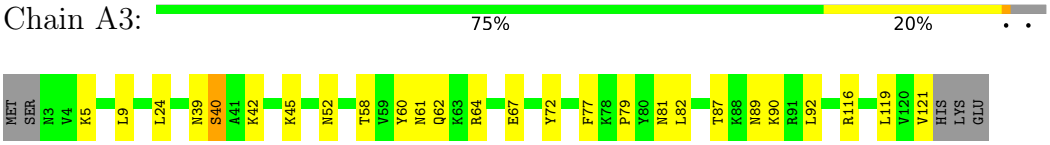
• Molecule 66: 60S ribosomal protein L26

Chain AZ:



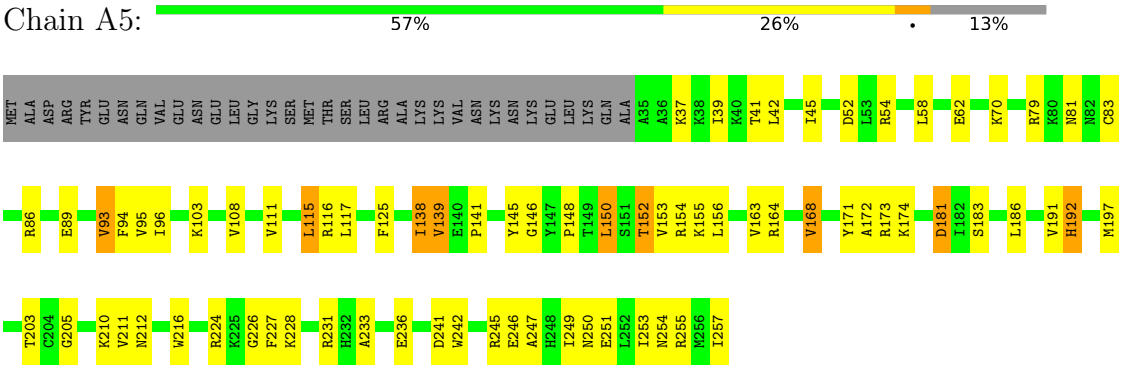
• Molecule 67: 60S ribosomal protein L35

Chain A3:



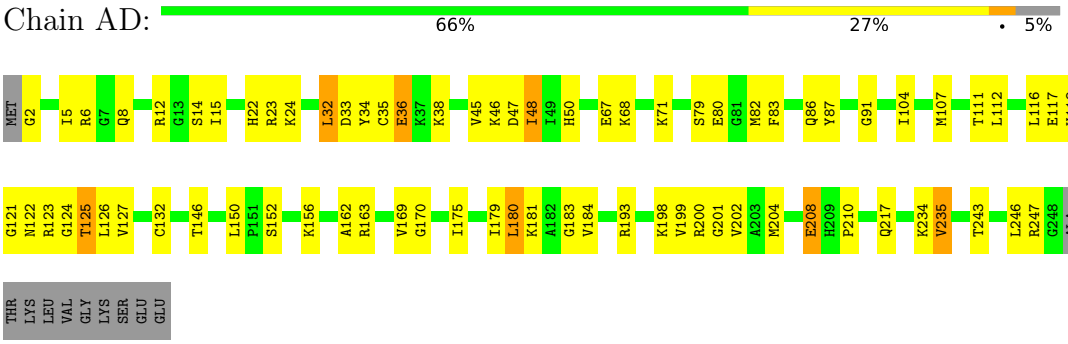
• Molecule 68: 60S ribosomal protein L7

Chain A5:



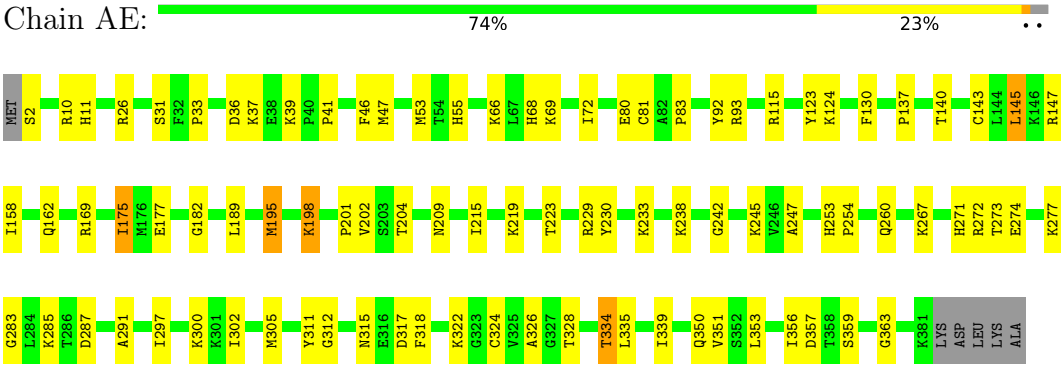
• Molecule 69: 60S ribosomal protein L2

Chain AD:



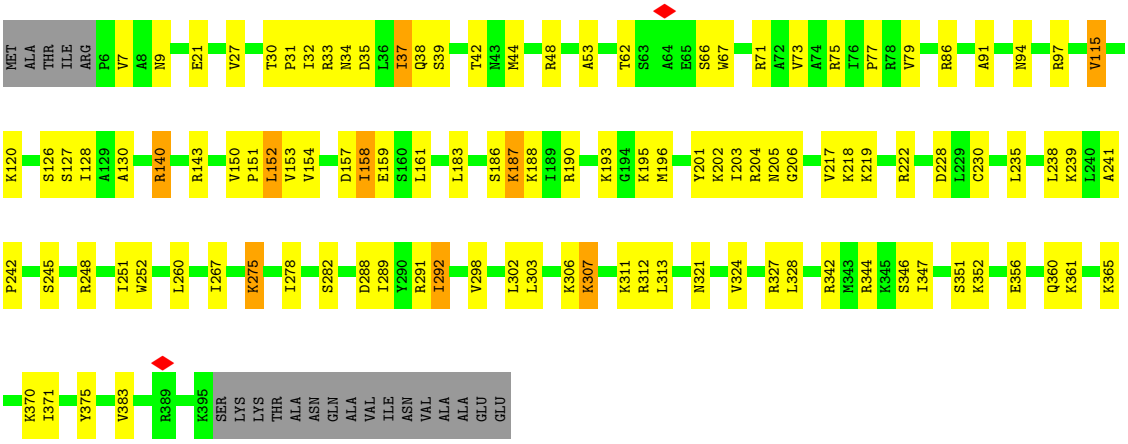
• Molecule 70: 60S ribosomal protein L3

Chain AE:



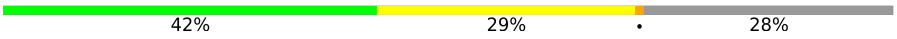
• Molecule 71: 60S ribosomal protein L4

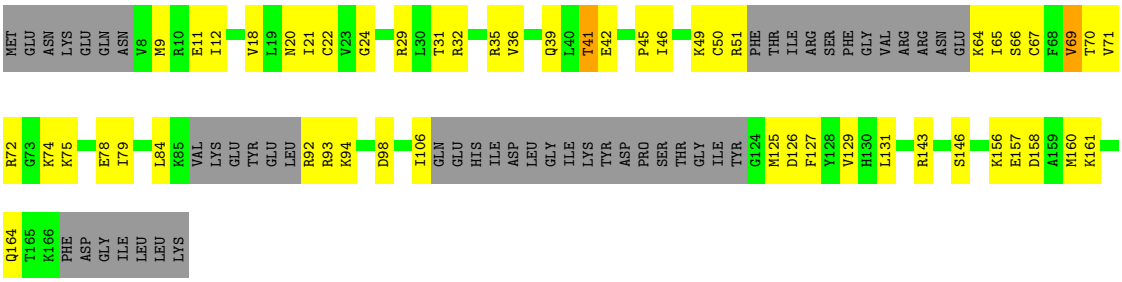
Chain AF:



• Molecule 72: 60S ribosomal protein L11a

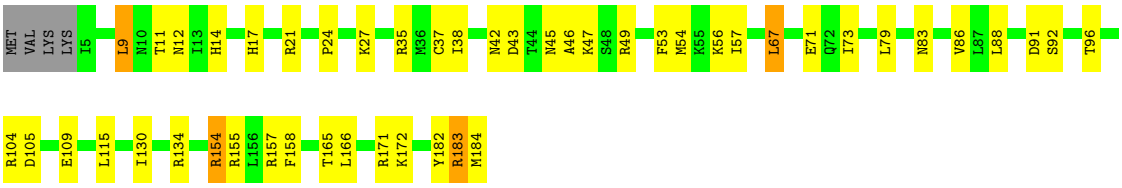
Chain AG:





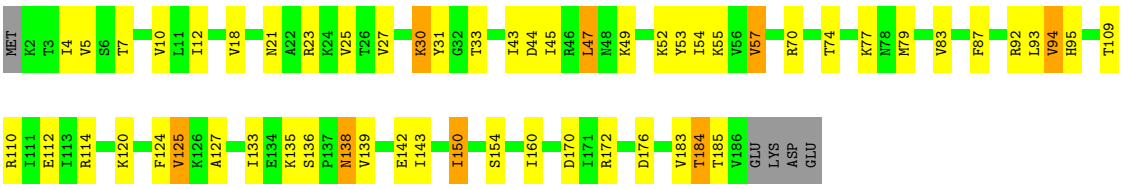
• Molecule 73: 60S ribosomal protein L18a

Chain AU:



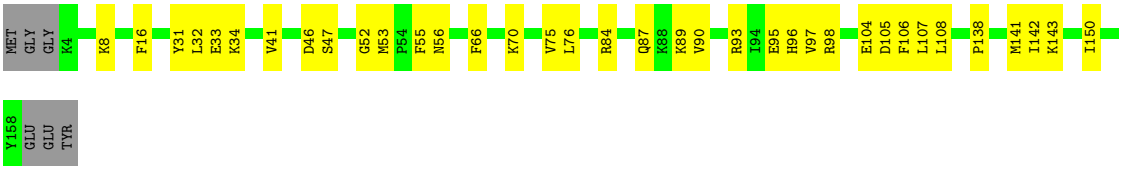
• Molecule 74: 60S ribosomal protein L6

Chain AH:



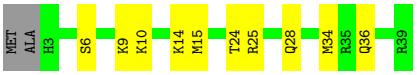
• Molecule 75: 60S ribosomal protein L21

Chain AV:



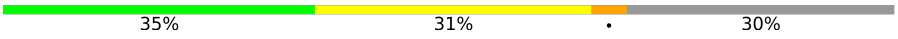
• Molecule 76: 60S ribosomal protein L41

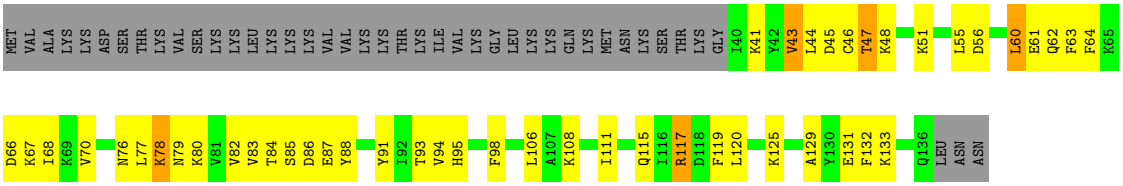
Chain Ag:



• Molecule 77: 60S ribosomal protein L22

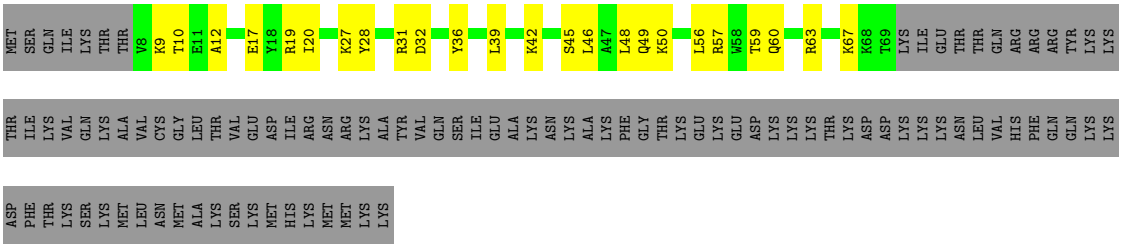
Chain AX:





• Molecule 78: 60S ribosomal protein L24

Chain A0:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	248063	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	60	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.096	Depositor
Minimum map value	-0.024	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.00547	Depositor
Map size (Å)	415.0, 415.0, 415.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83, 0.83, 0.83	Depositor

5 Model quality

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	S1	0.23	0/998	0.47	0/1321
2	S2	0.08	0/323	0.26	0/435
3	S3	0.25	0/793	0.43	0/1055
4	S4	0.19	0/597	0.50	0/801
5	S5	0.14	0/466	0.38	0/616
6	S6	0.19	0/348	0.45	0/458
7	S7	0.18	0/1754	0.28	0/2732
8	SA	0.25	0/38276	0.29	0/59598
9	SB	0.26	0/1737	0.46	0/2321
10	SC	0.24	0/1569	0.51	0/2129
11	SD	0.15	0/1240	0.37	0/1652
12	SE	0.24	0/1538	0.44	0/2055
13	SF	0.24	0/2097	0.43	0/2819
14	SG	0.26	0/1799	0.46	0/2429
15	SH	0.20	0/1668	0.39	0/2214
16	SI	0.15	0/1443	0.39	0/1936
17	SJ	0.19	0/1544	0.43	0/2064
18	SK	0.28	0/1054	0.49	0/1411
19	SL	0.27	0/1407	0.51	0/1879
20	SM	0.17	0/1113	0.43	0/1487
21	SN	0.14	0/780	0.37	0/1053
22	SO	0.11	0/705	0.34	0/950
23	SP	0.26	0/966	0.50	0/1295
24	SQ	0.25	0/1149	0.39	0/1532
25	SR	0.09	0/754	0.29	0/1013
26	SS	0.19	0/1062	0.59	2/1425 (0.1%)
27	ST	0.13	0/412	0.35	0/544
28	SU	0.25	0/1223	0.41	0/1634
29	SV	0.27	0/1233	0.41	0/1645
30	SW	0.20	0/792	0.53	0/1053
31	SX	0.14	0/787	0.39	0/1050
32	SY	0.14	0/1294	0.33	0/1742
33	SZ	0.25	0/565	0.48	0/758
34	AA	0.34	0/75947	0.33	0/118255

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
35	AC	0.34	0/3599	0.33	0/5603
36	AB	0.30	0/2816	0.28	0/4388
37	AL	0.29	0/1793	0.40	0/2387
38	A1	0.27	0/1151	0.47	1/1531 (0.1%)
39	A2	0.26	0/846	0.43	0/1124
40	A4	0.27	0/564	0.40	0/737
41	A6	0.29	0/748	0.39	0/1001
42	A7	0.29	0/805	0.36	0/1073
43	AN	0.29	0/1226	0.44	0/1632
44	A8	0.31	0/1053	0.45	0/1399
45	A9	0.35	0/864	0.45	0/1160
46	Aa	0.31	0/862	0.42	0/1148
47	Ab	0.26	0/762	0.45	0/1008
48	Ad	0.28	0/611	0.55	0/812
49	Ae	0.29	0/396	0.29	0/521
50	Af	0.28	0/418	0.37	0/556
51	AP	0.35	0/1735	0.49	0/2320
52	Ah	0.31	0/667	0.37	0/887
53	Ai	0.30	0/788	0.37	0/1032
54	AI	0.28	0/1708	0.43	0/2274
55	AJ	0.24	0/1840	0.47	0/2456
56	Ac	0.32	0/722	0.46	0/951
57	AK	0.31	0/1689	0.41	0/2260
58	AM	0.30	0/1012	0.41	0/1363
59	AS	0.32	0/1531	0.43	0/2040
60	AO	0.32	0/1199	0.44	0/1597
61	AQ	0.22	0/1579	0.40	0/2113
62	AR	0.26	0/2078	0.40	0/2776
63	AW	0.31	0/1244	0.45	0/1663
64	AY	0.27	0/805	0.41	0/1074
65	AT	0.30	0/1525	0.46	0/2016
66	AZ	0.29	0/1012	0.48	0/1339
67	A3	0.26	0/1004	0.36	0/1329
68	A5	0.31	0/1917	0.43	1/2562 (0.0%)
69	AD	0.33	0/1901	0.44	0/2544
70	AE	0.31	0/3129	0.38	0/4195
71	AF	0.30	0/3144	0.40	0/4205
72	AG	0.24	0/1020	0.49	0/1349
73	AU	0.32	0/1527	0.41	0/2043
74	AH	0.28	0/1500	0.40	0/2025
75	AV	0.29	0/1300	0.39	0/1732
76	Ag	0.25	0/348	0.39	0/448
77	AX	0.27	0/841	0.52	0/1125

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
78	A0	0.30	0/533	0.43	0/711
All	All	0.29	0/207245	0.36	4/303870 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
26	SS	102	ALA	CB-CA-C	-6.90	108.62	116.63
38	A1	19	ALA	CB-CA-C	-5.86	109.81	116.54
68	A5	246	GLU	CB-CA-C	-5.77	109.94	116.63
26	SS	102	ALA	N-CA-C	5.71	117.74	108.08

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	S1	985	0	1076	65	0
2	S2	320	0	338	9	0
3	S3	781	0	820	31	0
4	S4	586	0	604	31	0
5	S5	465	0	505	24	0
6	S6	345	0	381	12	0
7	S7	1571	0	797	61	0
8	SA	34208	0	17266	831	0
9	SB	1713	0	1838	64	0
10	SC	1538	0	1600	91	0
11	SD	1228	0	1311	55	0
12	SE	1514	0	1605	71	0
13	SF	2061	0	2200	96	0
14	SG	1757	0	1811	65	0
15	SH	1651	0	1807	70	0
16	SI	1424	0	1471	62	0
17	SJ	1528	0	1680	59	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	SK	1037	0	1099	33	0
19	SL	1383	0	1434	59	0
20	SM	1098	0	1183	63	0
21	SN	772	0	813	44	0
22	SO	686	0	695	21	0
23	SP	954	0	997	51	0
24	SQ	1129	0	1196	33	0
25	SR	746	0	754	14	0
26	SS	1046	0	1101	87	0
27	ST	405	0	419	30	0
28	SU	1202	0	1299	52	0
29	SV	1206	0	1239	38	0
30	SW	785	0	858	68	0
31	SX	776	0	832	28	0
32	SY	1266	0	1316	58	0
33	SZ	557	0	558	23	0
34	AA	67884	0	34243	1148	0
35	AC	3215	0	1633	58	0
36	AB	2517	0	1275	57	0
37	AL	1761	0	1896	50	0
38	A1	1134	0	1245	42	0
39	A2	837	0	896	17	0
40	A4	555	0	599	12	0
41	A6	740	0	763	26	0
42	A7	793	0	869	14	0
43	AN	1210	0	1329	47	0
44	A8	1036	0	1139	35	0
45	A9	844	0	886	22	0
46	Aa	850	0	904	30	0
47	Ab	756	0	842	25	0
48	Ad	603	0	686	22	0
49	Ae	388	0	421	6	0
50	Af	413	0	452	10	0
51	AP	1697	0	1802	68	0
52	Ah	658	0	727	21	0
53	Ai	778	0	861	19	0
54	AI	1685	0	1849	62	0
55	AJ	1813	0	1985	64	0
56	Ac	709	0	761	31	0
57	AK	1659	0	1782	57	0
58	AM	996	0	1044	29	0
59	AS	1503	0	1636	29	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
60	AO	1172	0	1230	41	0
61	AQ	1544	0	1582	55	0
62	AR	2049	0	2145	70	0
63	AW	1319	0	1303	29	0
64	AY	796	0	850	30	0
65	AT	1509	0	1682	36	0
66	AZ	1000	0	1099	42	0
67	A3	994	0	1121	19	0
68	A5	1879	0	2005	60	0
69	AD	1866	0	1964	58	0
70	AE	3061	0	3205	68	0
71	AF	3094	0	3333	88	0
72	AG	1010	0	1073	38	0
73	AU	1497	0	1556	38	0
74	AH	1475	0	1574	38	0
75	AV	1275	0	1355	23	0
76	Ag	343	0	388	9	0
77	AX	824	0	882	35	0
78	A0	521	0	539	18	0
All	All	192985	0	144314	4451	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 13.

The worst 5 of 4451 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:AA:10:G:H21	34:AA:1706:A:N6	1.31	1.27
34:AA:10:G:N2	34:AA:1706:A:H61	1.38	1.20
34:AA:11:A:N6	35:AC:154:G:H1	1.40	1.19
7:S7:29:G:H1	7:S7:38:A:N6	1.42	1.17
36:AB:22:G:N2	36:AB:25:A:C6	2.23	1.05

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	S1	118/133 (89%)	114 (97%)	4 (3%)	0	100	100
2	S2	35/105 (33%)	35 (100%)	0	0	100	100
3	S3	93/107 (87%)	86 (92%)	7 (8%)	0	100	100
4	S4	74/82 (90%)	62 (84%)	12 (16%)	0	100	100
5	S5	55/67 (82%)	49 (89%)	5 (9%)	1 (2%)	6	9
6	S6	41/58 (71%)	39 (95%)	2 (5%)	0	100	100
9	SB	208/262 (79%)	197 (95%)	10 (5%)	1 (0%)	24	37
10	SC	193/263 (73%)	176 (91%)	16 (8%)	1 (0%)	24	37
11	SD	149/221 (67%)	146 (98%)	3 (2%)	0	100	100
12	SE	183/189 (97%)	170 (93%)	12 (7%)	1 (0%)	24	37
13	SF	255/261 (98%)	239 (94%)	15 (6%)	1 (0%)	30	43
14	SG	222/272 (82%)	211 (95%)	11 (5%)	0	100	100
15	SH	200/306 (65%)	188 (94%)	12 (6%)	0	100	100
16	SI	176/195 (90%)	161 (92%)	15 (8%)	0	100	100
17	SJ	186/194 (96%)	172 (92%)	13 (7%)	1 (0%)	24	37
18	SK	127/130 (98%)	116 (91%)	10 (8%)	1 (1%)	16	25
19	SL	165/218 (76%)	152 (92%)	11 (7%)	2 (1%)	10	16
20	SM	136/144 (94%)	132 (97%)	3 (2%)	1 (1%)	18	28
21	SN	96/118 (81%)	92 (96%)	4 (4%)	0	100	100
22	SO	77/137 (56%)	74 (96%)	2 (3%)	1 (1%)	9	14
23	SP	125/151 (83%)	110 (88%)	15 (12%)	0	100	100
24	SQ	142/145 (98%)	135 (95%)	7 (5%)	0	100	100
25	SR	92/141 (65%)	88 (96%)	4 (4%)	0	100	100
26	SS	126/156 (81%)	103 (82%)	21 (17%)	2 (2%)	7	11
27	ST	46/54 (85%)	44 (96%)	2 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
28	SU	147/151 (97%)	137 (93%)	10 (7%)	0	100 100
29	SV	142/161 (88%)	135 (95%)	5 (4%)	2 (1%)	9 13
30	SW	91/137 (66%)	82 (90%)	7 (8%)	2 (2%)	5 6
31	SX	92/145 (63%)	84 (91%)	8 (9%)	0	100 100
32	SY	152/170 (89%)	145 (95%)	7 (5%)	0	100 100
33	SZ	70/82 (85%)	66 (94%)	4 (6%)	0	100 100
37	AL	209/215 (97%)	199 (95%)	10 (5%)	0	100 100
38	A1	136/146 (93%)	124 (91%)	10 (7%)	2 (2%)	8 12
39	A2	97/127 (76%)	90 (93%)	7 (7%)	0	100 100
40	A4	64/67 (96%)	59 (92%)	5 (8%)	0	100 100
41	A6	96/108 (89%)	93 (97%)	3 (3%)	0	100 100
42	A7	92/120 (77%)	91 (99%)	1 (1%)	0	100 100
43	AN	145/165 (88%)	134 (92%)	11 (8%)	0	100 100
44	A8	123/131 (94%)	111 (90%)	12 (10%)	0	100 100
45	A9	101/140 (72%)	95 (94%)	6 (6%)	0	100 100
46	Aa	104/150 (69%)	95 (91%)	9 (9%)	0	100 100
47	Ab	91/112 (81%)	84 (92%)	7 (8%)	0	100 100
48	Ad	68/87 (78%)	67 (98%)	1 (2%)	0	100 100
49	Ae	39/51 (76%)	38 (97%)	1 (3%)	0	100 100
50	Af	49/128 (38%)	45 (92%)	4 (8%)	0	100 100
51	AP	202/205 (98%)	183 (91%)	16 (8%)	3 (2%)	8 12
52	Ah	83/96 (86%)	81 (98%)	2 (2%)	0	100 100
53	Ai	93/104 (89%)	90 (97%)	3 (3%)	0	100 100
54	AI	203/221 (92%)	192 (95%)	9 (4%)	2 (1%)	12 20
55	AJ	216/283 (76%)	205 (95%)	10 (5%)	1 (0%)	24 37
56	Ac	87/92 (95%)	76 (87%)	11 (13%)	0	100 100
57	AK	199/202 (98%)	192 (96%)	6 (3%)	1 (0%)	24 37
58	AM	130/139 (94%)	122 (94%)	7 (5%)	1 (1%)	16 25
59	AS	184/187 (98%)	175 (95%)	8 (4%)	1 (0%)	24 37
60	AO	145/148 (98%)	136 (94%)	8 (6%)	1 (1%)	18 28
61	AQ	185/219 (84%)	167 (90%)	16 (9%)	2 (1%)	11 18

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
62	AR	244/294 (83%)	232 (95%)	11 (4%)	1 (0%)	30	43
63	AW	149/173 (86%)	141 (95%)	8 (5%)	0	100	100
64	AY	99/190 (52%)	93 (94%)	6 (6%)	0	100	100
65	AT	179/182 (98%)	177 (99%)	2 (1%)	0	100	100
66	AZ	119/126 (94%)	112 (94%)	7 (6%)	0	100	100
67	A3	117/124 (94%)	111 (95%)	6 (5%)	0	100	100
68	A5	221/257 (86%)	205 (93%)	16 (7%)	0	100	100
69	AD	245/260 (94%)	232 (95%)	11 (4%)	2 (1%)	16	25
70	AE	378/386 (98%)	366 (97%)	11 (3%)	1 (0%)	36	50
71	AF	388/411 (94%)	368 (95%)	19 (5%)	1 (0%)	36	50
72	AG	116/173 (67%)	107 (92%)	9 (8%)	0	100	100
73	AU	178/184 (97%)	169 (95%)	9 (5%)	0	100	100
74	AH	183/190 (96%)	170 (93%)	13 (7%)	0	100	100
75	AV	153/161 (95%)	149 (97%)	4 (3%)	0	100	100
76	Ag	35/39 (90%)	29 (83%)	6 (17%)	0	100	100
77	AX	95/139 (68%)	91 (96%)	3 (3%)	1 (1%)	11	18
78	A0	60/162 (37%)	59 (98%)	1 (2%)	0	100	100
All	All	10114/12049 (84%)	9495 (94%)	582 (6%)	37 (0%)	31	43

5 of 37 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	SB	146	ARG
17	SJ	112	ILE
20	SM	41	GLU
26	SS	101	ILE
29	SV	41	VAL

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	S1	104/115 (90%)	98 (94%)	6 (6%)	18 32
2	S2	35/88 (40%)	35 (100%)	0	100 100
3	S3	87/98 (89%)	84 (97%)	3 (3%)	32 54
4	S4	70/76 (92%)	67 (96%)	3 (4%)	26 44
5	S5	48/54 (89%)	46 (96%)	2 (4%)	26 45
6	S6	36/47 (77%)	32 (89%)	4 (11%)	6 9
9	SB	195/238 (82%)	180 (92%)	15 (8%)	12 20
10	SC	167/227 (74%)	160 (96%)	7 (4%)	26 45
11	SD	132/188 (70%)	128 (97%)	4 (3%)	36 58
12	SE	161/167 (96%)	150 (93%)	11 (7%)	14 25
13	SF	233/237 (98%)	219 (94%)	14 (6%)	17 31
14	SG	191/222 (86%)	177 (93%)	14 (7%)	13 22
15	SH	182/279 (65%)	174 (96%)	8 (4%)	25 43
16	SI	154/165 (93%)	150 (97%)	4 (3%)	40 63
17	SJ	177/183 (97%)	167 (94%)	10 (6%)	19 33
18	SK	115/116 (99%)	103 (90%)	12 (10%)	7 10
19	SL	151/193 (78%)	140 (93%)	11 (7%)	13 22
20	SM	116/122 (95%)	111 (96%)	5 (4%)	26 44
21	SN	91/109 (84%)	86 (94%)	5 (6%)	19 34
22	SO	76/129 (59%)	74 (97%)	2 (3%)	40 63
23	SP	99/119 (83%)	95 (96%)	4 (4%)	28 47
24	SQ	120/121 (99%)	114 (95%)	6 (5%)	22 38
25	SR	83/121 (69%)	82 (99%)	1 (1%)	63 81
26	SS	114/136 (84%)	109 (96%)	5 (4%)	25 43
27	ST	43/48 (90%)	43 (100%)	0	100 100
28	SU	132/133 (99%)	123 (93%)	9 (7%)	14 25
29	SV	131/144 (91%)	122 (93%)	9 (7%)	14 24
30	SW	86/127 (68%)	84 (98%)	2 (2%)	44 66
31	SX	88/130 (68%)	86 (98%)	2 (2%)	44 66
32	SY	137/151 (91%)	129 (94%)	8 (6%)	18 32
33	SZ	60/70 (86%)	56 (93%)	4 (7%)	15 26
37	AL	190/194 (98%)	178 (94%)	12 (6%)	16 29

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
38	A1	127/132 (96%)	114 (90%)	13 (10%)	7 11
39	A2	98/118 (83%)	93 (95%)	5 (5%)	21 37
40	A4	60/61 (98%)	60 (100%)	0	100 100
41	A6	83/92 (90%)	76 (92%)	7 (8%)	10 17
42	A7	90/112 (80%)	86 (96%)	4 (4%)	25 43
43	AN	136/152 (90%)	129 (95%)	7 (5%)	21 37
44	A8	114/120 (95%)	106 (93%)	8 (7%)	14 24
45	A9	90/127 (71%)	85 (94%)	5 (6%)	19 33
46	Aa	88/128 (69%)	83 (94%)	5 (6%)	18 33
47	Ab	82/97 (84%)	73 (89%)	9 (11%)	6 9
48	Ad	69/83 (83%)	65 (94%)	4 (6%)	18 32
49	Ae	40/48 (83%)	39 (98%)	1 (2%)	42 64
50	Af	45/114 (40%)	44 (98%)	1 (2%)	45 67
51	AP	179/180 (99%)	166 (93%)	13 (7%)	13 22
52	Ah	70/80 (88%)	67 (96%)	3 (4%)	26 44
53	Ai	87/93 (94%)	85 (98%)	2 (2%)	44 66
54	AI	189/203 (93%)	172 (91%)	17 (9%)	9 15
55	AJ	204/260 (78%)	193 (95%)	11 (5%)	20 35
56	Ac	74/77 (96%)	68 (92%)	6 (8%)	11 18
57	AK	181/182 (100%)	170 (94%)	11 (6%)	17 30
58	AM	106/110 (96%)	99 (93%)	7 (7%)	15 26
59	AS	158/159 (99%)	151 (96%)	7 (4%)	25 43
60	AO	121/122 (99%)	116 (96%)	5 (4%)	27 46
61	AQ	165/190 (87%)	154 (93%)	11 (7%)	15 26
62	AR	215/254 (85%)	208 (97%)	7 (3%)	33 55
63	AW	128/131 (98%)	124 (97%)	4 (3%)	35 57
64	AY	90/177 (51%)	83 (92%)	7 (8%)	11 20
65	AT	162/163 (99%)	153 (94%)	9 (6%)	19 33
66	AZ	111/115 (96%)	105 (95%)	6 (5%)	20 35
67	A3	110/115 (96%)	105 (96%)	5 (4%)	24 42
68	A5	201/231 (87%)	189 (94%)	12 (6%)	17 31

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
69	AD	191/202 (95%)	177 (93%)	14 (7%)	13 22
70	AE	335/340 (98%)	325 (97%)	10 (3%)	36 58
71	AF	336/352 (96%)	319 (95%)	17 (5%)	21 37
72	AG	110/155 (71%)	103 (94%)	7 (6%)	16 28
73	AU	162/166 (98%)	156 (96%)	6 (4%)	30 51
74	AH	168/173 (97%)	155 (92%)	13 (8%)	12 20
75	AV	140/144 (97%)	132 (94%)	8 (6%)	18 33
76	Ag	34/35 (97%)	34 (100%)	0	100 100
77	AX	92/131 (70%)	82 (89%)	10 (11%)	6 9
78	A0	53/146 (36%)	50 (94%)	3 (6%)	18 33
All	All	9098/10617 (86%)	8596 (94%)	502 (6%)	21 34

5 of 502 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
43	AN	6	LEU
71	AF	127	SER
52	Ah	64	VAL
71	AF	37	ILE
74	AH	94	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 77 such sidechains are listed below:

Mol	Chain	Res	Type
63	AW	147	GLN
73	AU	131	ASN
65	AT	130	GLN
69	AD	122	ASN
77	AX	75	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	AA	3163/3788 (83%)	636 (20%)	69 (2%)
35	AC	148/159 (93%)	33 (22%)	5 (3%)
36	AB	117/119 (98%)	18 (15%)	3 (2%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
7	S7	73/74 (98%)	20 (27%)	0
8	SA	1587/2092 (75%)	349 (21%)	29 (1%)
All	All	5088/6232 (81%)	1056 (20%)	106 (2%)

5 of 1056 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
7	S7	8	U
7	S7	9	G
7	S7	10	G
7	S7	16	U
7	S7	17	U

5 of 106 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
34	AA	715	U
34	AA	1705	A
35	AC	37	A
34	AA	764	G
34	AA	1217	U

5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
63	AW	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AW	154:ASN	C	197:UNK	N	31.36

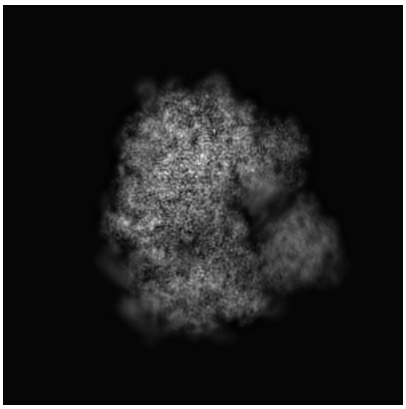
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-44918. These allow visual inspection of the internal detail of the map and identification of artifacts.

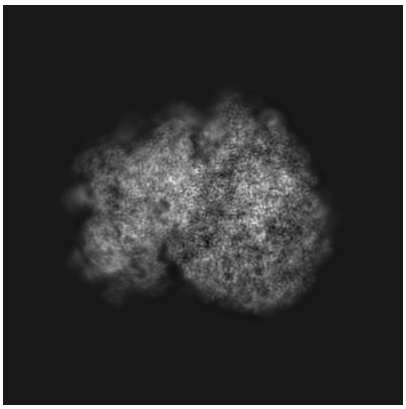
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

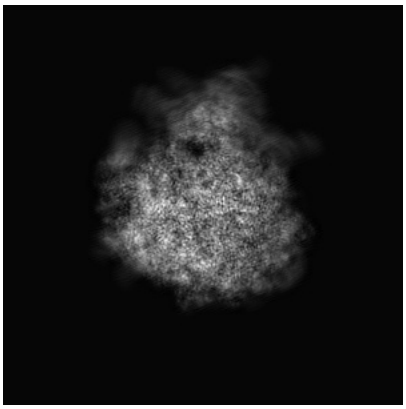
6.1.1 Primary map



X

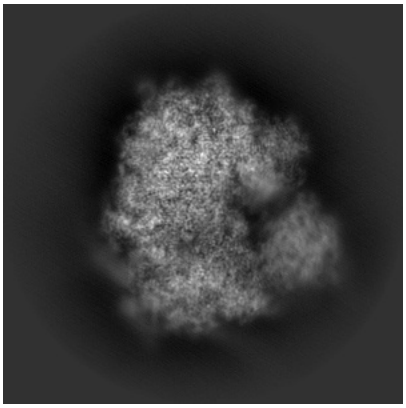


Y

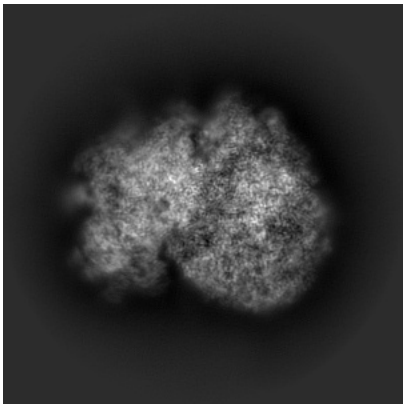


Z

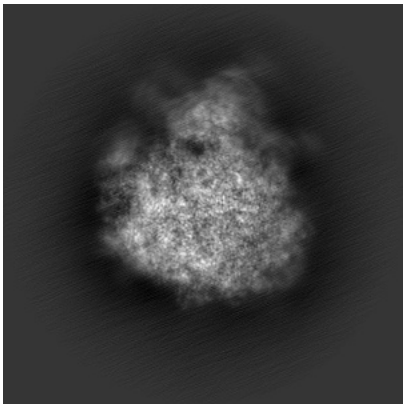
6.1.2 Raw map



X



Y

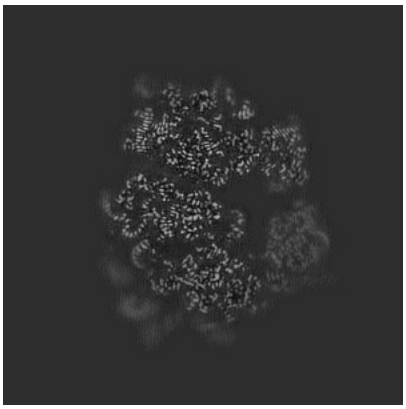


Z

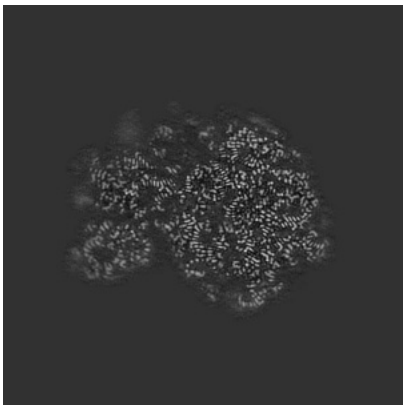
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

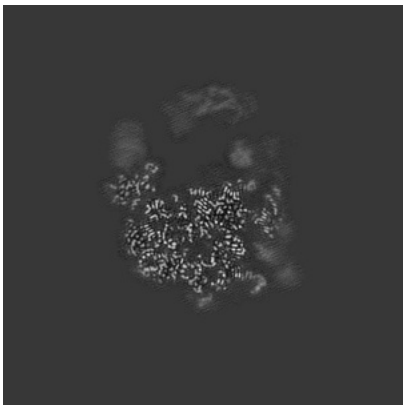
6.2.1 Primary map



X Index: 250

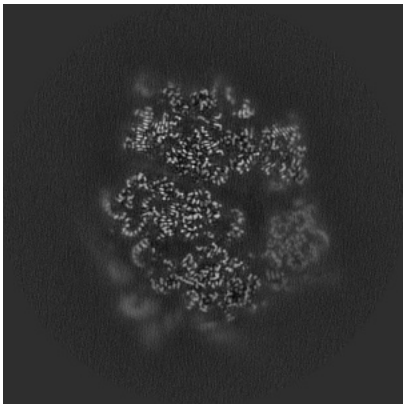


Y Index: 250

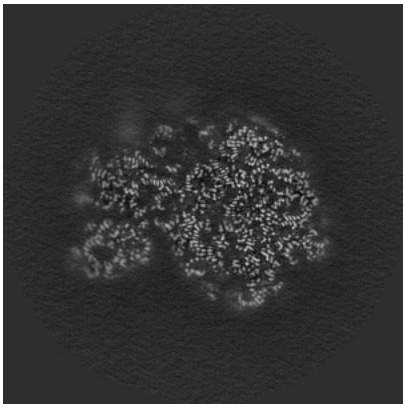


Z Index: 250

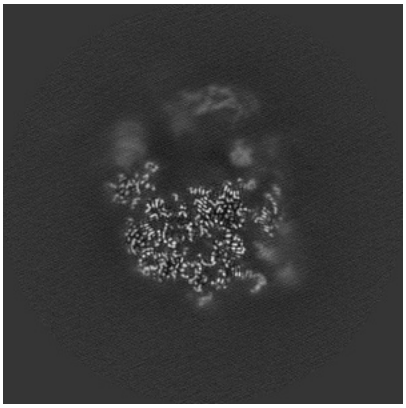
6.2.2 Raw map



X Index: 250



Y Index: 250



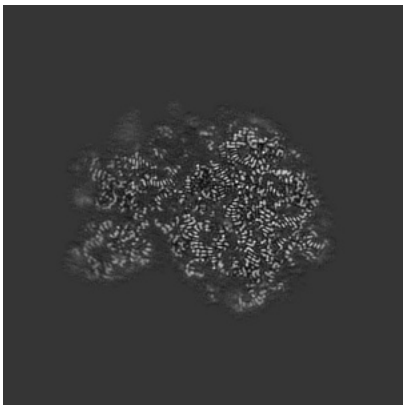
Z Index: 250

The images above show central slices of the map in three orthogonal directions.

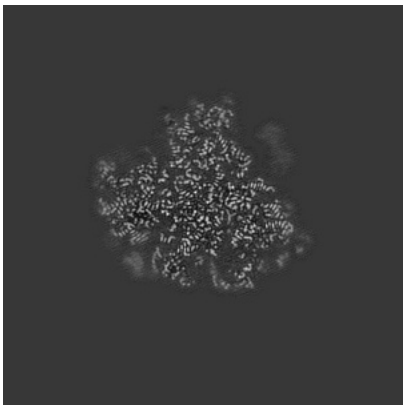
6.3 Largest variance slices (i)

6.3.1 Primary map

X Index: 275

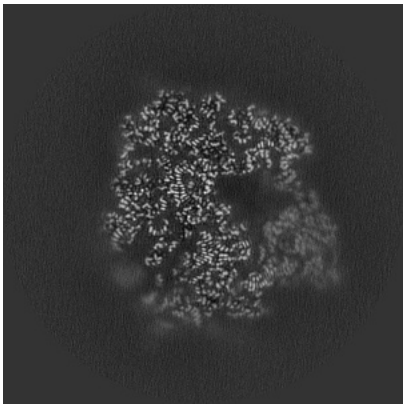


Y Index: 249

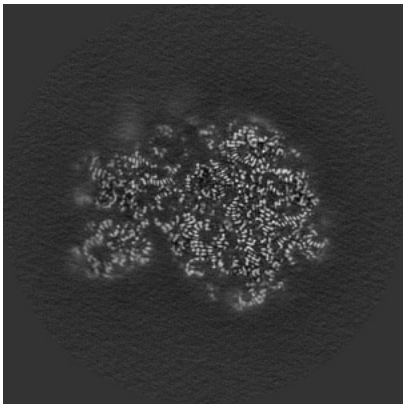


Z Index: 311

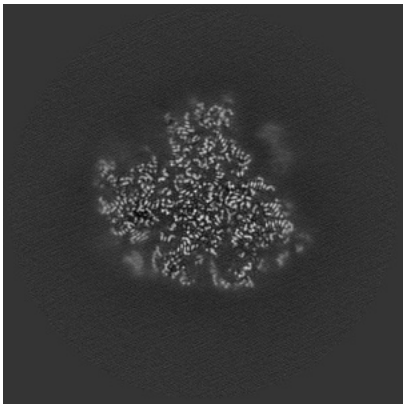
6.3.2 Raw map



X Index: 275



Y Index: 249

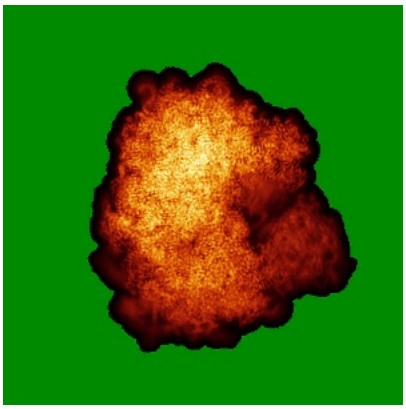


Z Index: 311

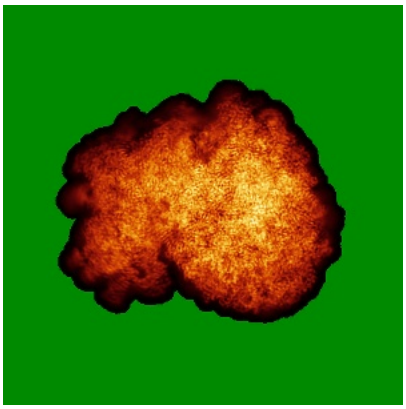
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

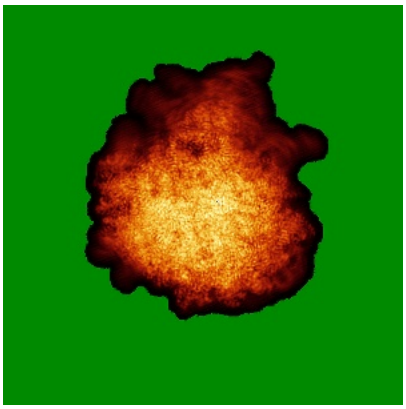
6.4.1 Primary map



X

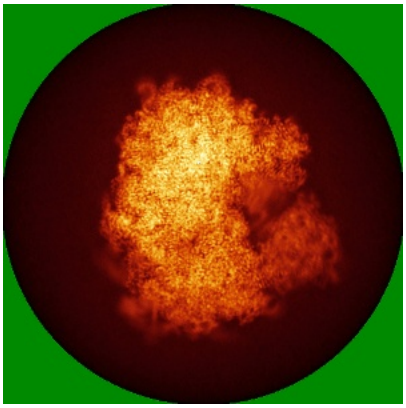


Y

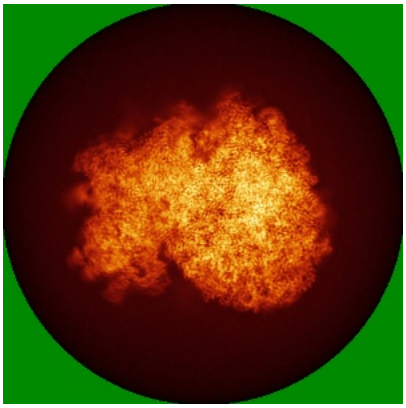


Z

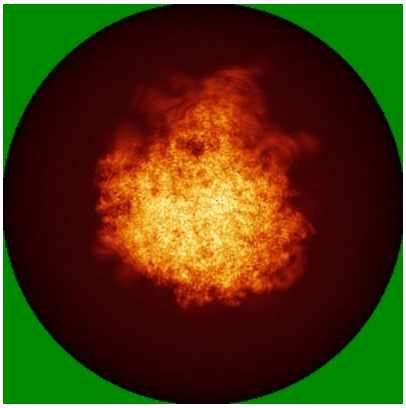
6.4.2 Raw map



X



Y

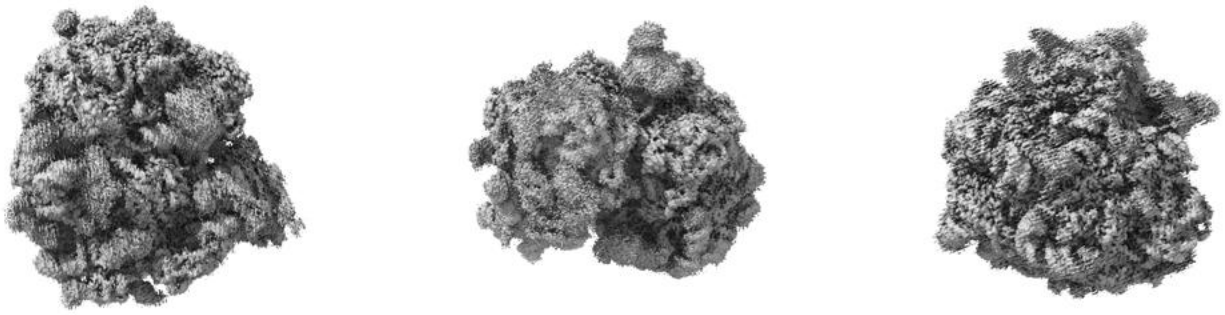


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views (i)

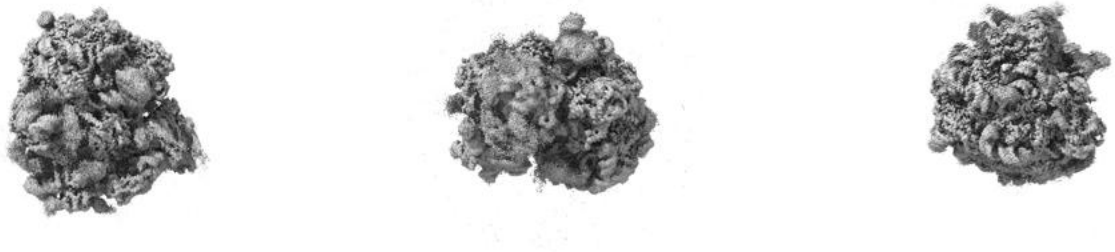
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.00547. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

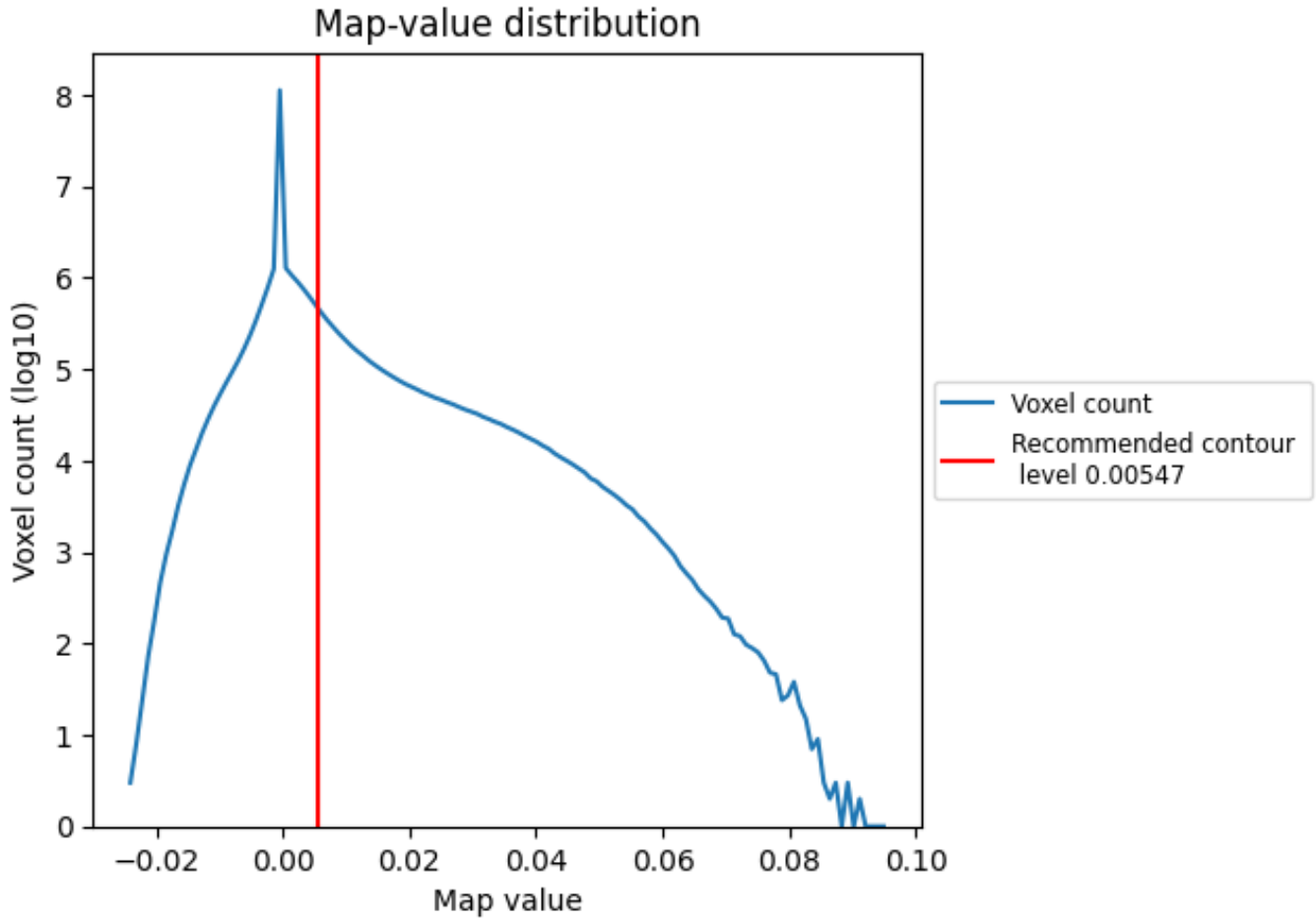
6.6 Mask visualisation (i)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis

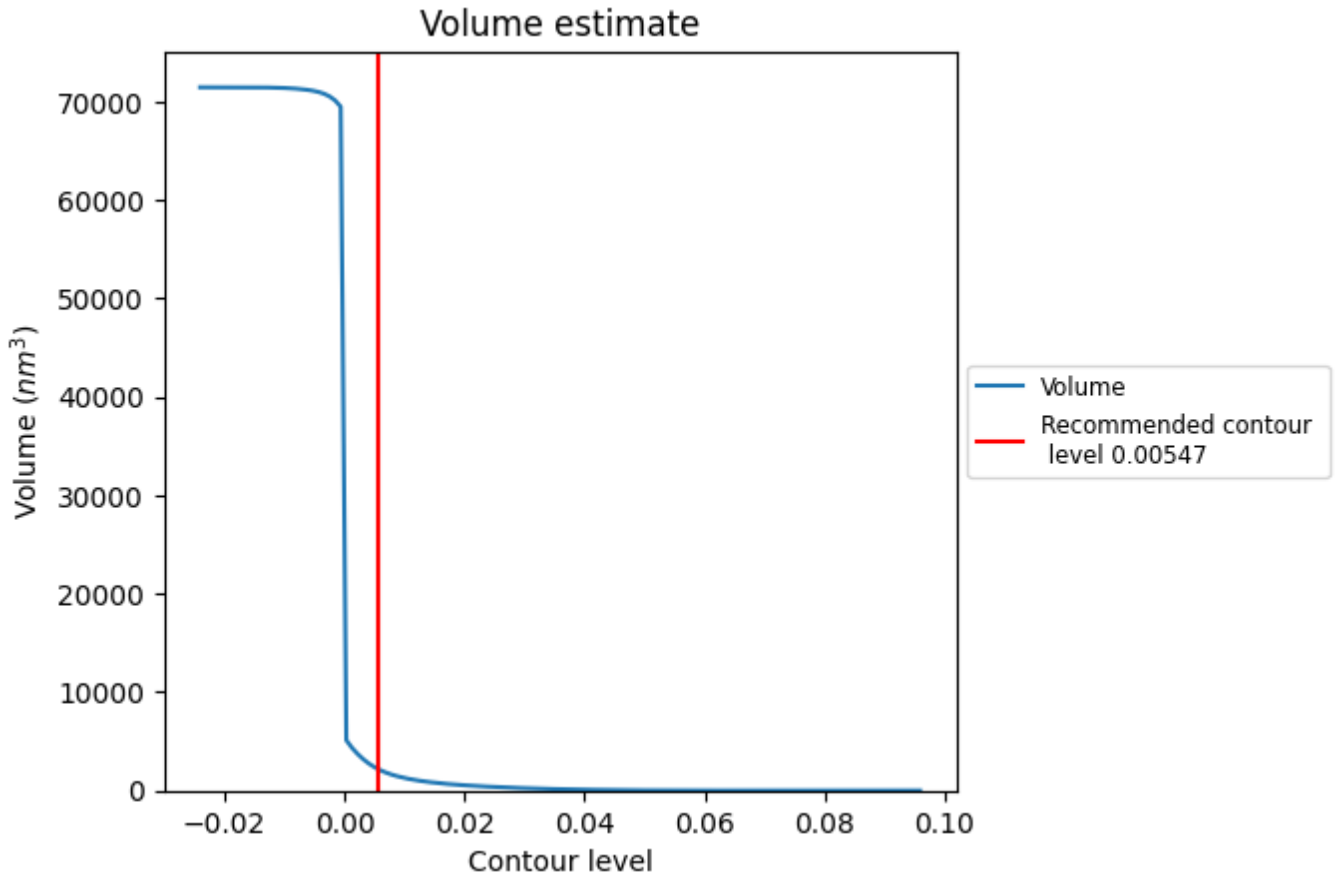
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

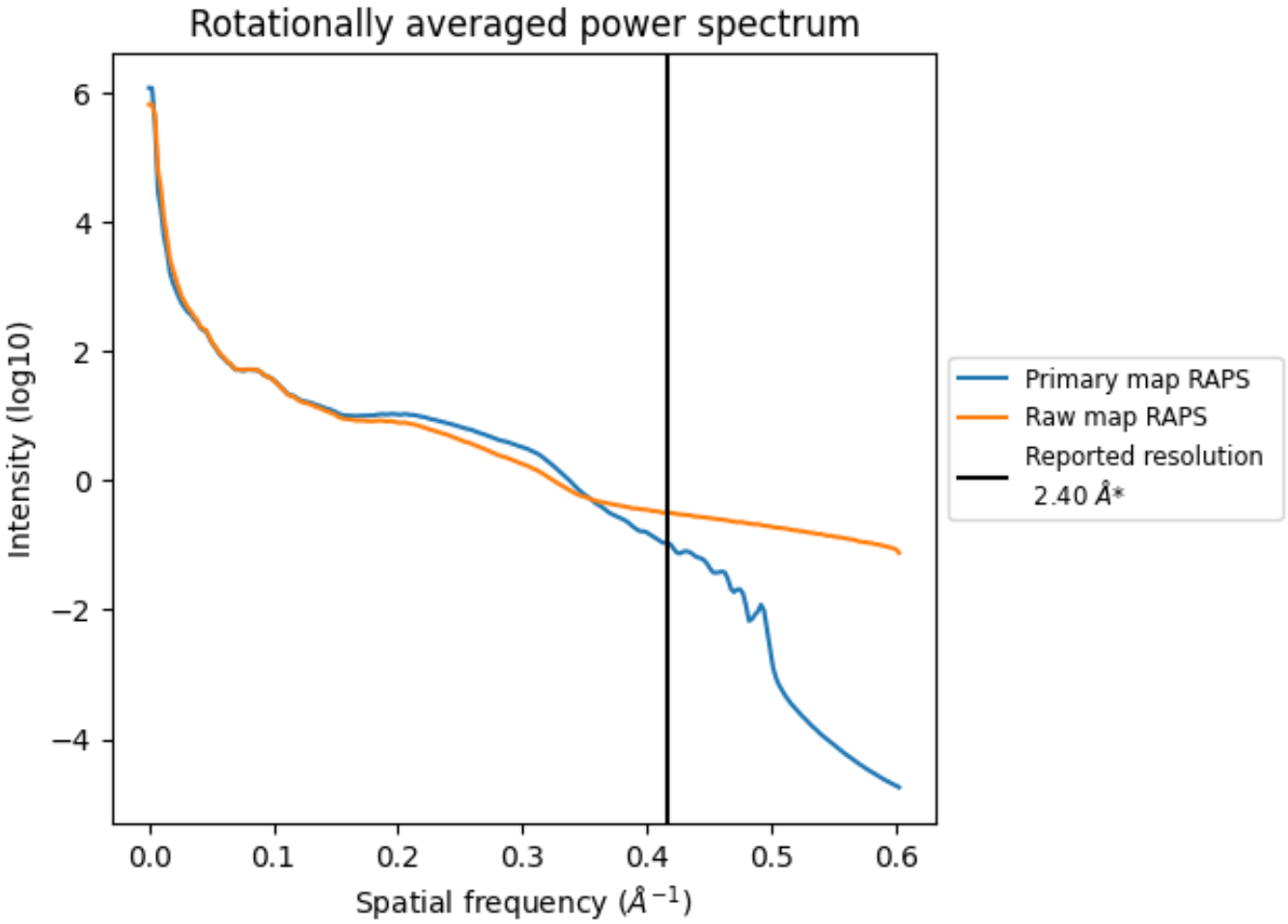
7.2 Volume estimate (i)



The volume at the recommended contour level is 2225 nm^3; this corresponds to an approximate mass of 2010 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)

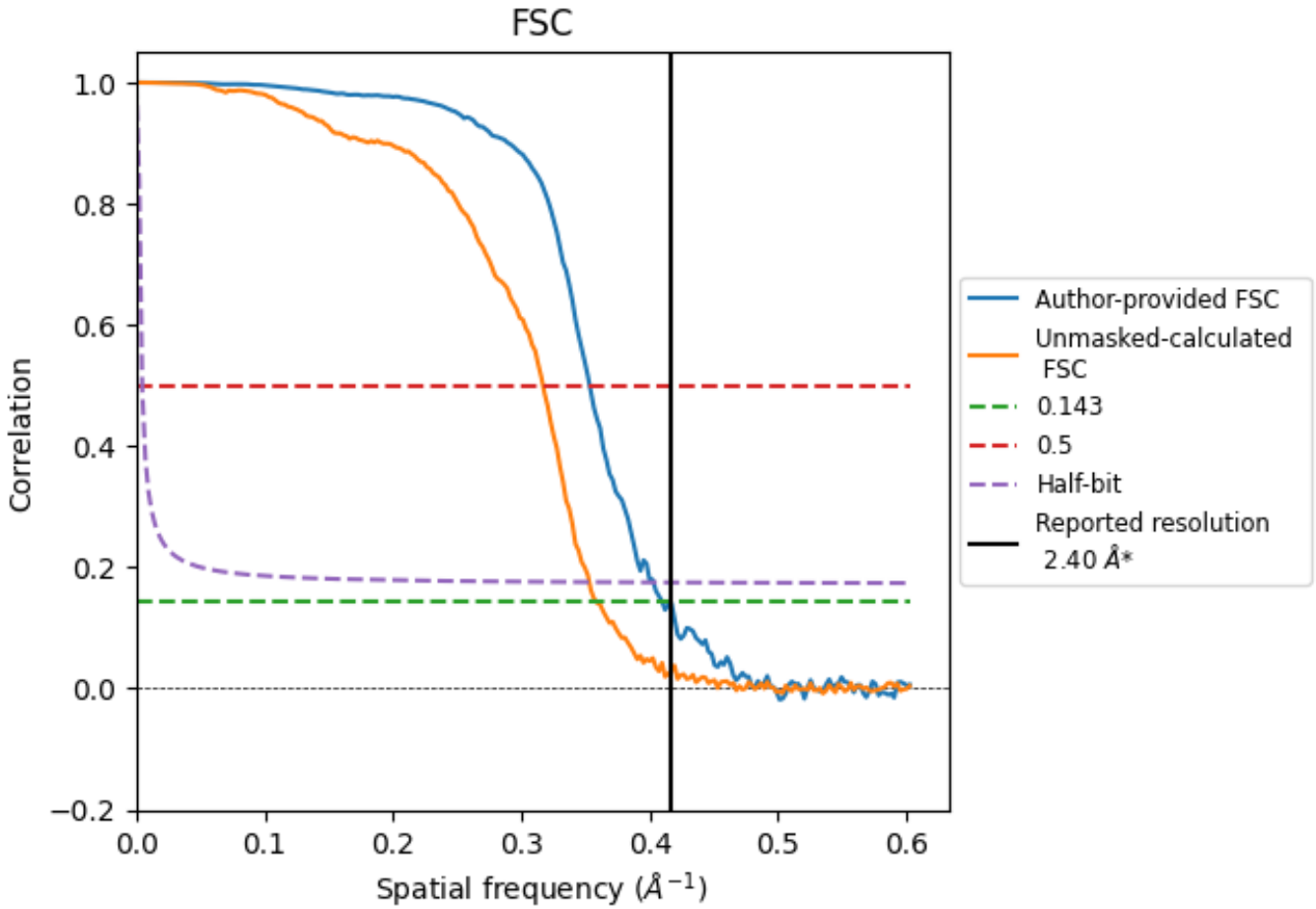


*Reported resolution corresponds to spatial frequency of 0.417 Å^{-1}

8 Fourier-Shell correlation

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC



*Reported resolution corresponds to spatial frequency of 0.417 Å^{-1}

8.2 Resolution estimates (i)

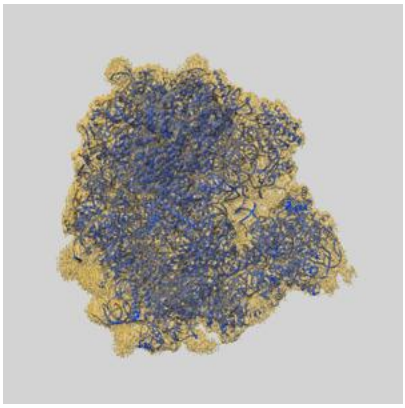
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.40	-	-
Author-provided FSC curve	2.44	2.83	2.48
Unmasked-calculated*	2.79	3.16	2.83

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 2.79 differs from the reported value 2.4 by more than 10 %

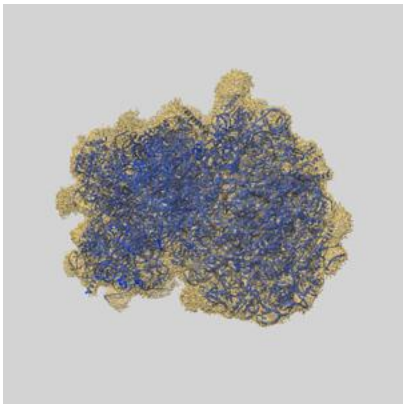
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-44918 and PDB model 9BUS. Per-residue inclusion information can be found in section 3 on page 18.

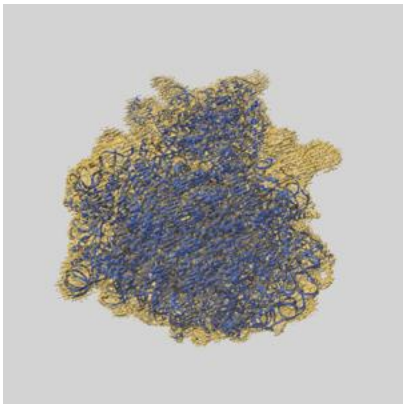
9.1 Map-model overlay



X



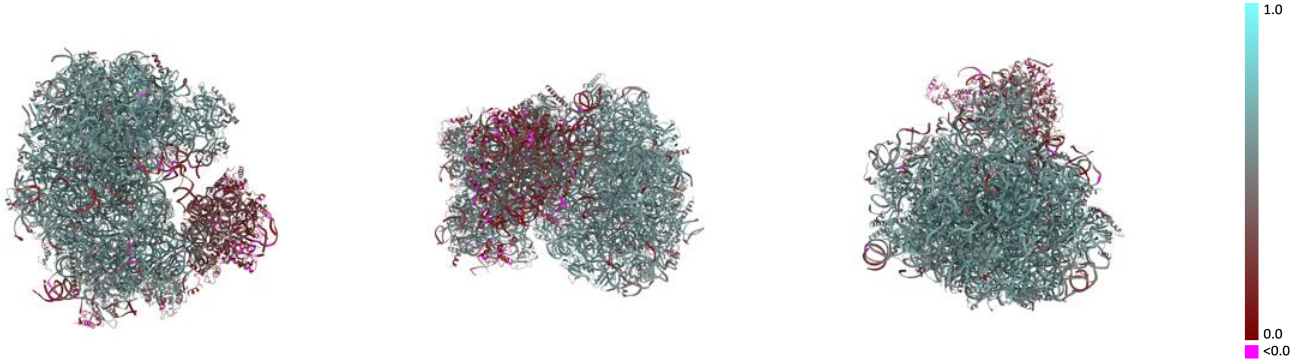
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.00547 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

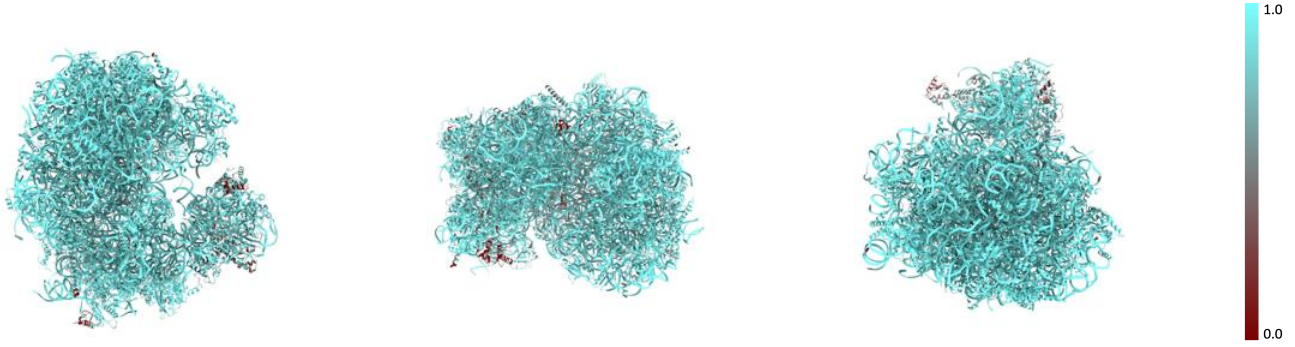
9.2 Q-score mapped to coordinate model



X Y Z

The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

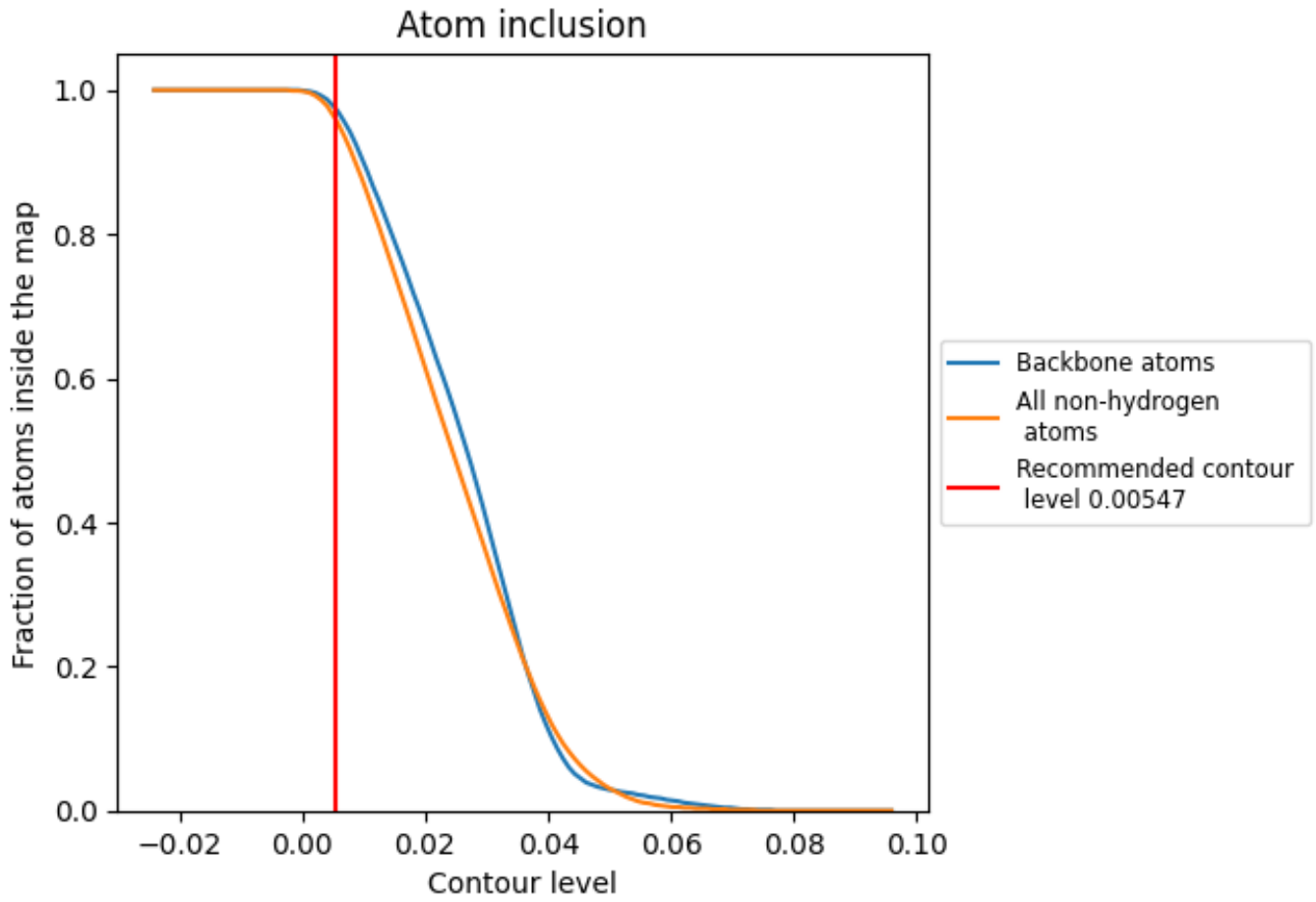
9.3 Atom inclusion mapped to coordinate model



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.00547).

9.4 Atom inclusion (i)



At the recommended contour level, 97% of all backbone atoms, 96% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.00547) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9590	0.5550
A0	0.9460	0.6110
A1	0.9530	0.5420
A2	0.9720	0.6020
A3	0.9770	0.6050
A4	0.9120	0.5490
A5	0.9700	0.6290
A6	0.9530	0.5830
A7	0.9780	0.6330
A8	0.9700	0.6360
A9	0.9890	0.6560
AA	0.9910	0.6120
AB	0.9940	0.6160
AC	0.9980	0.6270
AD	0.9780	0.6480
AE	0.9860	0.6470
AF	0.9420	0.5950
AG	0.9610	0.5130
AH	0.9850	0.6140
AI	0.9720	0.5820
AJ	0.9150	0.5200
AK	0.9800	0.6350
AL	0.9820	0.6230
AM	0.9790	0.6360
AN	0.9620	0.5870
AO	0.9820	0.6510
AP	0.9830	0.6480
AQ	0.9380	0.5630
AR	0.9610	0.5670
AS	0.9800	0.6500
AT	0.9140	0.5760
AU	0.9840	0.6300
AV	0.9780	0.6230
AW	0.9850	0.6440
AX	0.9470	0.5180

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Chain	Atom inclusion	Q-score
AY	0.9500	0.5780
AZ	0.9750	0.5750
Aa	0.9620	0.6100
Ab	0.9670	0.5880
Ac	0.9810	0.6400
Ad	0.9710	0.5730
Ae	0.9840	0.6220
Af	0.9830	0.6220
Ag	0.9310	0.5980
Ah	0.9810	0.6500
Ai	0.9720	0.6430
S1	0.9130	0.4760
S2	0.2600	0.1370
S3	0.9690	0.5910
S4	0.8090	0.3900
S5	0.7740	0.2740
S6	0.9100	0.4830
S7	0.9100	0.2460
SA	0.9810	0.4990
SB	0.9300	0.5330
SC	0.9300	0.4880
SD	0.7020	0.2270
SE	0.9180	0.5240
SF	0.9480	0.5600
SG	0.9510	0.5520
SH	0.9100	0.4310
SI	0.7970	0.2350
SJ	0.7810	0.3890
SK	0.9650	0.6000
SL	0.9490	0.5740
SM	0.7660	0.2110
SN	0.6980	0.2070
SO	0.7390	0.1490
SP	0.9440	0.5510
SQ	0.9340	0.5720
SR	0.3180	0.0740
SS	0.7690	0.1760
ST	0.7450	0.2980
SU	0.9280	0.5760
SV	0.9560	0.6080
SW	0.8070	0.2510
SX	0.6910	0.1630

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
SY	0.8710	0.2330
SZ	0.9520	0.5360